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Title: Modulating developmental pathways in plants.

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The invention relates to a method to modulate plant growth or development by modifying genes in plants. The invention among others relates to modifying RKS genes or gene products as found in *Arabidopsis thaliana* or other plants. The different domains of RKS gene products essentially have the following functions: The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain et al. 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine / proline rich region. The next domain displays all the characteristics of a single transmembrane domain. At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine /threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062, WO 01/29240). The kinase domain is followed by a domain with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

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Plant homologs of the Arabidopsis RKS genes can be found by comparison of various plant database (see also Table 2) and comprise amongst others:

- 5 Y14600|SBRLK1|*Sorghum bicolor*
BF004020|BF004020|EST432518 KV1 *Medicago truncatata*
AW934655|AW934655|EST353547 tomato
AW617954|AW617954|EST314028 *L. pennellii*
AA738544|AA738544|SbRLK2 *Sorghum bicolor*
- 10 AA738545|AA738545|SbRLK3 *Sorghum bicolor*
BG595415|BG595415|EST494093 cSTS *Solanum tuberosa*
AI896277|AI896277|EST265720 tomato
BF643238|BF643238|NF002H05EC1F1045
AA738546|AA738546|SbRLK4 *Sorghum bicolor*
- 15 BE658174|BE658174|GM700005A20D5 Gm-r1070 *Glycine max*
BF520845|BF520845|EST458318 DSIL *Medicago truncata*
AC069324|AC069324|*Oryza sativa*
AW761055|AW761055|sl70d06.y1 Gm-cl027 *Glycine max*
BE352622|BE352622|WHE0425_G11_M21ZS Wheat
- 20 BG647340|BG647340|EST508959 HOGA *Medicago truncata*
AY028699|AY028699|*Brassica napus*
AW666082|AW666082|sk31h04.y1 Gm-cl028 *Glycine max*
AA738547|AA738547|SbRLK5 *Sorghum bicolor*
BG127658|BG127658|EST473220 tomato
- 25 L27821|RICPRKI|*Oryza sativa*
BG238468|BG238468|sab51a09.y1 Gm-cl043 *Glycine max*
BG441204|BG441204|GA_Ea0012C15f *Gossypium arbo.*
AW667985|AW667985|GA_Ea0012C15 *Gossypium arbore.*
AW233982|AW233982|sf32g05.y1 Gm-cl028 *Glycine max*
- 30 AP003235|AP003235|*Oryza sativa*
BF460294|BF460294|074A05 Mature tuber
AY007545|AY007545|*Brassica napus*
AC087544|AC087544|*Oryza sativa*
AB041503|AB041503|*Populus nigra*

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The invention furthermore relates to modifying ELS genes or gene products or functional equivalents thereof which are for example derived from at least two different genes in the

40 Arabidopsis genome. They show high homology on protein level

with the corresponding transmembrane RKS gene products.
 However, they lack a transmembrane domain while they do
 contain a signaling sequence at the N-terminal end. Therefore
 these proteins are thought to be positioned within vesicles
 5 within the plant cell or at the outside of the plasma
 membrane, within the cell wall of the plant cell. A number of
 homologs have been detected in other plant species, such as:

- AF370543|AF370543|*Arabidopsis thaliana*
 10 AF324989|AF324989|*Arabidopsis thaliana*
AV520367|AV520367|*Arabidopsis thaliana*
AV553051|AV553051|*Arabidopsis thaliana*
BF642233|BF642233|NF050C09IN1F1069
AW559436|AW559436|EST314484 *DSIR Medicago truncata*
 15 BG456991|BG456991|NF099F02PL1F1025
AW622146|AW622146|EST312944 tomato
BF260895|BF260895|HVSMEf0023D15f *Hordeum vulgare*
BE322325|BE322325|NF022E12IN1F1088
BG414774|BG414774|HVSMEk0003K21f *Hordeum vulgare*
 20 BE460627|BE460627|EST412046 tomato
BI204894|BI204894|EST522934 *ctOS Lycopersicon esculentum*
BI205306|BI205306|EST523346 *ctOS Lycopersicon esculentum*
BI204366|BI204366|EST522406 *ctOS Lycopersicon esculentum*
AW443205|AW443205|EST308135 tomato
 25 AW031110|AW031110|EST274417 tomato
BI180080|BI180080|EST521025 *cSTE Solanum tuberosa*
BF644761|BF644761|NF015A11EC1F1084
AV526127|AV526127|*Arabidopsis thaliana*
AV556193|AV556193|*Arabidopsis thaliana*
 30 BE203316|BE203316|EST403338 *KV1 Medicago truncatata*.
AW649615|AW649615|EST328069 tomato
BE512465|BE512465|946071E06
BI204917|BI204917|EST522957 *ctOS Lycopersicon esculentum*
BG590749|BG590749|EST498591
 35 BG648725|BG648725|EST510344 *HOGA Medicago truncata*
BG648619|BG648619|EST510238 *HOGA Medicago truncata*
BG597757|BG597757|EST496435 *cSTS Solanum tuberosa*
AW221939|AW221939|EST298750 tomato
BE704836|BE704836|Sc01_
 40 BG124409|BG124409|EST470055 tomato

- BF051954 | BF051954 | EST437120 tomato
BG320355 | BG320355 | Zm03_05h01_Zea mays
AV526624 | AV526624 | Arabidopsis thaliana
AW933960 | AW933960 | EST359803 tomato
- 5 AW221278 | AW221278 | EST297747 tomato
BE405514 | BE405514 | WHE1212_C01_F02ZS Wheat
BG314461 | BG314461 | WHE2495_A12_A23ZS Triticum
BF258673 | BF258673 | HVSMEf0016G01f *Hordeum vulgare*
BG262637 | BG262637 | WHE0938_E03_I06ZS Wheat
- 10 AW030188 | AW030188 | EST273443 tomato
BG653580 | BG653580 | sad76b11.y1 Gm-cl051 *Glycine max*
BG319729 | BG319729 | Zm03_05h01_A Zm03_Zea mays
BF053590 | BF053590 | EST438820 potato
BE454808 | BE454808 | HVSMEh0095C03f *Hordeum vulgare*
- 15 BI075801 | BI075801 | IP1_21_D05.b1_A002
BE367593 | BE367593 | PI1_9_F02.b1_A002 *Sorghum bicolor*
2e-074 BF260080 | BF260080 | HVSMEf0021A22f *Hordeum vulgare*
BF627921 | BF627921 | HVSMEb0006I23f *Hordeum vulgare*
BG598491 | BG598491 | EST503391 cSTS *Solanum tuberosa*
- 20 AW038168 | AW038168 | EST279825 tomato
BG343258 | BG343258 | HVSMEg0005D23f *Hordeum vulgare*
AW925684 | AW925684 | HVSMEg0005D23 *Hordeum vulgare*
BG416093 | BG416093 | HVSMEk0009L18f *Hordeum vulgare*
AW683370 | AW683370 | NF011C09LF1F1069
- 25 BE420108 | BE420108 | WWS020.C1R000101 ITEC WWS Wheat
AW350720 | AW350720 | GM210009A10F4 Gm-r1021 *Glycine max*
AW616564 | AW616564 | EST322975 *L. Hirsutum trichome*
AW011134 | AW011134 | ST17B03 Pine
BF630746 | BF630746 | HVSMEb0013N06f *Hordeum vulgare*
- 30 AW926045 | AW926045 | HVSMEg0006C10 *Hordeum vulgare*
BE519800 | BE519800 | HV_CEb0021E12f *Hordeum vulgare*
BG343657 | BG343657 | HVSMEg0006C10f *Hordeum vulgare*
BG933682 | BG933682 | OV1_16_C09.b1_A002
BE433368 | BE433368 | EST399897 tomato
- 35 AW219797 | AW219797 | EST302279 tomato
BF629324 | BF629324 | HVSMEb0010N06f *Hordeum vulgare*
BE597128 | BE597128 | PI1_71_A07.g1_A002
AW220075 | AW220075 | EST302558 tomato
AW616639 | AW616639 | EST323050 *L. Hirsutum trichome*
- 40 BF645214 | BF645214 | NF032F11EC1F1094
AW924540 | AW924540 | WS1_70_H12.b1_A002

- AI775448|AI775448|EST256548 tomato
AW983360|AW983360|HVSMEg0010F15f *Hordeum vulgare*
BF270171|BF270171|GA_Eb0007B13f *Gossypium arbor.*
BE919631|BE919631|EST423400 potato
- 5 AW037836|AW037836|EST279465 tomato
BF008781|BF008781|ss79h09.y1 Gm-cl064 *Glycine max*
BF254651|BF254651|HVSMEf0004K05f *Hordeum vulgare*
BE599797|BE599797|PI1_79_H01.g1_A002
BE599026|BE599026|PI1_86_E03.g1_A002
- 10 R89998|R89998|16353 Lambda-PRL2 *Arabidopsis*
BG841108|BG841108|MEST15-G02.T3 ISUM4-TN *Zea mays*
AW307218|AW307218|sf54c07.y1 Gm-cl009 *Glycine max*
AI496325|AI496325|sb05c09.y1 Gm-cl004 *Glycine max*
AJ277703|ZMA277703|*Zea mays*
- 15 AL375586|CNS0616P|*Medicago truncatula* EST
AW350549|AW350549|GM210009A10A12 Gm-r1021 *Glycine max*
BE125918|BE125918|DG1_59_F02.b1_A002
BF053901|BF053901|EST439131 potato
BE921389|BE921389|EST425266 potato
- 20 BE597551|BE597551|PI1_71_A07.b1
BE360092|BE360092|DG1_61_C09.b1_A002
BE660084|BE660084|491 GmaxSC *Glycine max*
AJ277702|ZMA277702|*Zea mays*
- 25 The invention also relates to modifying SBP/SPL gene or
 products which represent a family of transcription factors
 with a bipartite nuclear localization signal (The SQUAMOSA
 PROMOTER-BINDING PROTEIN-LIKE (SBP/SPL) gene family of
Arabidopsis thaliana, Columbia ecotype). Upon activation
- 30 (probably by RKS mediated phosphorylation, the bipartite
 nuclear localization signal becomes linear and available for
 the nuclear translocation of the protein. Within the plant
 nucleus, the transcription factor regulates transcription by
 interaction with specific promoter elements. .In *Arabidopsis*
- 35 *thaliana*, this family is represented by at least 16 different
 members (see following list). In many other plant species, we
 also identified members of this transcription factor family
 (See list on page 7).

Functional interaction between RKS and SBP proteins was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter (data not shown). At the tip of double overexpressing plants, embryo structures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signalling cascade, resulting in the reprogramming of developmental fate of a determined meristem. (ref. dissertation: <http://www.ub.uni-koeln.de/ediss/archiv/2001/11wl204.pdf>; Plant Journal 1997: 12, 2 367-377; Mol. Gen. Genet. 1996: 250, 7-16; Gene 1999, 237, 91-104, Genes and Development 1997: 11, 616-628), Proc. Natl. Acad. Sci. USA 1998: 95, 10306-10311; The Plant Journal 2000: 22, 523-529; Science 1997: 278, 1963-1965; Plant Physiol. Biochem. 2000: 38, 789-796; Cell 1996: 84, 61-71; Annu. Rev. Plant Physiol. Plant Mol. Biol. 1999: 50, 505-537

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	name	genetic code
	ATSPL1	At2g47070*
	ATSPL2	At5g43270
	ATSPL3	At2g33810*
25	ATSPL4	At1g53160*
	ATSPL5	At3g15270
	ATSPL6	At1g69170
	ATSPL7	At5g18830
	ATSPL8	At1g02065
30	ATSPL9	At2g42200*
	ATSPL10	At1g27370*
	ATSPL11	At1g27360*
	ATSPL12	At3g60030
	ATSPL13	At5g50570
35	ATSPL14	At1g20980
	ATSPL15	At3g57920
	ATSPL16	At1g76580

* annotation in database not complete and/or correct

In many other plant species, we identified members of this transcription factor family, plant homologs of the Arabidopsis SBP/SPL proteins are for example:

- 5 AB023037|AB023037|*Arabidopsis thaliana*
BG789832|BG789832|sae56b07.y1 *Gm-cl051 Glycine max*
BG123992|BG123992|EST469638 *tomato*
BG595750|BG595750|EST494428 *cSTS Solanum tuberosum*
AF370612|AF370612|*Arabidopsis thaliana*
- 10 BF728335|BF728335|1000060H02.x1 1000 - *Zea mays*
X92079|AMSBP2|*A.majus*
AW331087|AW331087|707047A12.x1 707 - Mixed adult... 128 zea mays
AJ011643|ATH011643|*Arabidopsis thaliana*
L34039|RICRMSOA|*Oryza sativa*
- 15 AJ011638|ATH011638|*Arabidopsis thaliana*
AJ011639|ATH011639|*Arabidopsis thaliana*
AJ132096|ATH132096|*Arabidopsis thaliana*
BF482644|BF482644|WHE2301-2304_A21_A21ZS *Wheat*
BF202242|BF202242|WHE0984_D01_G02ZS *Wheat*
- 20 BE057470|BE057470|sm58e10.y1 *Gm-cl028 Glycine max*
AJ011628|ATH011628|*Arabidopsis thaliana*
AJ011629|ATH011629|*Arabidopsis thaliana*
AJ011617|ZMA011617|*Zea mays*
AJ011637|ATH011637|*Arabidopsis thaliana*
- 25 AJ011622|AMA011622|*Antirrhinum majus*
AJ011621|AMA011621|*Antirrhinum majus*
AJ011635|ATH011635|*Arabidopsis thaliana*
AJ011623|AMA011623|*Antirrhinum majus*
BF650908|BF650908|NF098D09EC1F1076
- 30 AJ242959|ATH242959|*Arabidopsis thaliana*
Y09427|ATSPL3|*A.thaliana* mRNA
AJ011633|ATH011633|*Arabidopsis thaliana*
AW691786|AW691786|NF044B06ST1F1000
BE058432|BE058432|sn16a06.y1 *Gm-cl016 Glycine max*
- 35 AW728623|AW728623|GA_Ea0017G06 *Gossypium arbore.*
BG442540|BG442540|GA_Ea0017G06f *Gossypium arbo.*
AJ011626|ATH011626|*Arabidopsis thaliana*
AJ011625|ATH011625|*Arabidopsis thaliana*
AI993858|AI993858|701515182 *A. thaliana*
- 40 BG593787|BG593787|EST492465 *cSTS Solanum tuberosum*
BF634536|BF634536|NF060C08DT1F1065 *Drought Medicago*

- BE806499|BE806499|ss59f10.y1 *Gm-cl062 Glycine max*
AW933950|AW933950|EST359793 *tomato*
AC008262|AC008262| *Arabidopsis*
B28493|B28493|T10A24TF *TAMU Arabidopsis thaliana*
- 5 AJ011644|ATH011644|*Arabidopsis thaliana*
AC018364|AC018364|*Arabidopsis thaliana*
AL092429|CNS00VLB|*Arabidopsis thaliana*
BE435668|BE435668|EST406746 *tomato*
BG097153|BG097153|EST461672 *potato*
- 10 BE440574|BE440574|sp47b09.y1 *Gm-cl043 Glycine max*
AI443033|AI443033|sa31a08.y1 *Gm-cl004 Glycine max*
U89496|ZMU89496|*Zea mays liguleless1*
AW433271|AW433271|sh54g07.y1 *Gm-cl015 Glycine max*
AW932595|AW932595|EST358438 *tomato*
- 15 AW096676|AW096676|EST289856 *tomato*
AJ011616|ZMA011616|*Zea mays*
AW036750|AW036750|EST252139 *tomato*
BF626329|BF626329|HVSMEa0018F24f *Hordeum vulgare*
AJ011614|ZMA011614|*Zea mays*
- 20 AJ011642|ATH011642|*Arabidopsis thaliana*
BE022435|BE022435|sm85h04.y1 *Gm-cl015 Glycine max*
X92369|AMSPB1|*A.majus*
AC015450|AC015450|*Arabidopsis thaliana*
AC079692|AC079692|*Arabidopsis thaliana*
- 25 AJ011632|ATH011632|*Arabidopsis thaliana*
AJ011631|ATH011631|*Arabidopsis thaliana*
BE455349|BE455349|HVSMEh0097E20f *Hordeum vulgare*
AJ242960|ATH242960|*Arabidopsis thaliana*
AJ011610|ATH011610|*Arabidopsis thaliana*
- 30 AJ132097|ATH132097|*Arabidopsis thaliana*
AL138658|ATT209|*Arabidopsis thaliana*
AJ011615|ZMA011615|*Zea mays*
BE499739|BE499739|WHE0975 *Wheat*
AW398794|AW398794|EST309294 *L. pennellii*
- 35 AJ011618|ZMA011618|*Zea mays*
AW747167|AW747167|WS1_66_F11.b1
AJ011577|ATH011577|*Arabidopsis thaliana*
AI992727|AI992727|701493410 *A. thaliana*
BE060783|BE060783|HVSMEg0013F15f *Hordeum vulgare*
- 40 BE804992|BE804992|ss34h10.y1 *Gm-cl061 Glycine max*
BE325341|BE325341|NF120H09ST1F1009

- AC007369|AC007369|*Arabidopsis thaliana*
AJ011619|ZMA011619|*Zea mays*
BI099345|BI099345|IP1_37_H10.b1_A002
BI071295|BI071295|C054P79U *Populus*
5 AZ920400|AZ920400|1006019G01.y2 1006 -
AZ919034|AZ919034|1006013G02.x3 1006 -
BE805023|BE805023|ss35d09.y1 Gm-cl061 *Glycine max*
BG582086|BG582086|EST483824 GVN *Medicago truncata*
AJ011609|ATH011609|*Arabidopsis thaliana*
10 BE023083|BE023083|sm90e08.y1 Gm-cl015 *Glycine max*

- Furthermore, the invention relates to modifying NDR-NHL-genes or gene products. All proteins belonging to this family contain one (and sometimes even more than one) transmembrane domain. *Arabidopsis* contains a large number of NDR-NHL genes, such as:
- 20 aad21459, aaf18257, aac36175, k10d20 (position 40852-41619),
aad21460, cab78082, aad21461, aad42003, aaf02134, aaf187656,
aaf02133, cab43430, cab88990, cab80950, aad25632, aaf23842, all63812,
f20d21-35, t13m11-12, fle22-7, t23g18, f5d14-4266, t32f12-16, f11f19-
11, f11f19-12, f11f19-13, t20p8-13, f12k2, f23h14, k10d20-44043,
k10d20-12, t19f11-6, t19f11-5, t10d17-10, f22o6-150, f3d13-5, m3e9-
80, t25p22-30, mhf15-4, mhf15-5, mrn17-4, mlf18-9, mgn6-11994, mjj3-
9667, f14f18-60, At1g17620 F11A6, At5g11890 , At2g27080 , At5g36970 ,
25 mlf18 , At1g65690 F1E22 , At4g01110 F2N1 , At2g35980 f11f19 ,
At4g01410 F3D13 , At1g54540 F20D21 , At2g46300 t3f17 , At5g21130 ,
At3g11650 T19F11 , At5g06320 MHF15 , At5g06330 MHF15 , At2g01080
f15b18 , At2g35460 t32f12 , At2g27260 f12k2 , At2g35970 f11f19 ,
At5g53730 MGN6 , At5g22870 MRN17 , At4g09590 , At3g54200 , At1g08160
30 T6D22 , At5g22200 , At3g52470 , At2g35960 f11f19 , At3g52460 ,
At5g56050 MDA7, At3g20590 K10D20 , At1g61760 T13M11 , At3g20600
K10D20 , At1g13050 F3F19 , At3g11660 T19F11 , At3g44220 , At1g64450
F1N19 , At3g26350 F20C19 C , At4g05220 , At5g45320 K9E15 ,
At4g23930 , At4g13270 , At4g39740 , At1g45688 F2G19 W , At5g42860
35 MBD2 , At1g32270 F27G20 , At4g30660 , At2g45430 f4l23 , At4g30650 ,
At1g69500 F10D13

and

- 40 ndr1, At2g27080; T20P8.13, At5g21130, At1g65690, At5g36970,

- At1g54540, At5g06320, At5g11890, At1g17620, At3g11650, At2g22180,
 At5g22870, At2g35980, At2g46300, At4g05220, At2g35460, At2g27260,
 At4g01410, At5g22200, At1g61760, At3g52470, At5g53730, At4g01110,
 At2g35960, At3g52460, At4g09590, At2g35970, At3g26350, At3g11660,
 5 At3g44220, At1g08160, At2g01080, At5g06330, At5g56050, At3g20600,
 NDR1, At3g54200, At3g20590, At4g39740, At1g32270 syntaxin, putative,
 At1g13050, At5g45320, At3g20610, At4g26490, At5g42860, At1g45688,
 At4g26820
- 10 NDR-NHL genes belong to a large family of which one of the
 first identified is the defence-associated gene HIN1 (Harpin-
 induced gene). HIN1 is transcriptionally induced by harpins
 and bacteria, that elicit hypersensitive responses in tobacco.
 It is thus believed that the genes of the invention also play
 15 arole in the hypersensitive reaction. Especially (see also
 chapter 8) since the genes of the invention bear relation to
 brassinoid-like responses and since brassinoid pathway
 compounds have been found to interact in this same defence
 system in plants. Other plant species also contain members of
 20 this large gene family, such as:

Plant homologs of the *Arabidopsis* NDR/NHL genes:

- 25 BG582276|BG582276|EST484016 GVN *Medicago truncata*
AV553539|AV553539|*Arabidopsis thaliana*
AC069325|AC069325|*Arabidopsis thaliana*
AV526693|AV526693|*Arabidopsis thaliana*
BG583456|BG583456|EST485208 GVN *Medicago truncata*
 30 AW267833|AW267833|EST305961 DSIR *Medicago truncata*
BE997791|BE997791|EST429514 GVSN *Medicago truncata*
BG580928|BG580928|EST482657 GVN *Medicago truncata*
BF520916|BF520916|EST458389 DSIL *Medicago truncata*
AV544651|AV544651|*Arabidopsis thaliana*
 35 AV543762|AV543762|*Arabidopsis thaliana*
AW559665|AW559665|EST314777 DSIR *Medicago truncata*
BG581012|BG581012|EST482741 GVN *Medicago truncata*
AV552164|AV552164|*Arabidopsis thaliana*
BE999881|BE999881|EST431604 GVSN *Medicago truncata*
 40 AW031098|AW031098|EST274405 tomato

- AI998763|AI998763|701546833 *A. thaliana*
AW219286|AW219286|EST301768 tomato
BE124562|BE124562|EST393597 GVN *Medicago truncata*
AV540371|AV540371|*Arabidopsis thaliana*
5 AV539549|AV539549|*Arabidopsis thaliana*
BG647432|BG647432|EST509051 HOGA *Medicago truncata*
BE434210|BE434210|EST405288 tomato
BG725849|BG725849|sae42g02.y1 Gm-cl051 *Glycine max*
AP003247|AP003247|*Oryza sativa*
10 BE348073|BE348073|spl1a11.y1 Gm-cl042 *Glycine max*
AW508383|AW508383|si40c06.y1 Gm-r1030 *Glycine max*
AI856504|AI856504|sb40b07.y1 Gm-cl014 *Glycine max*
BE556317|BE556317|sq01b07.y1 Gm-cl045 *Glycine max*
AA713120|AA713120|32681 *Arabidopsis*
15 AV541531|AV541531|*Arabidopsis thaliana*
AI894456|AI894456|EST263911 tomato
AW704493|AW704493|sk53g11.y1 Gm-cl019 *Glycine max*
AW219298|AW219298|EST301780 tomato
BF425685|BF425685|ss03c11.y1 Gm-cl047 *Glycine max*
20 AV422557|AV422557|*Lotus japonicus*
BE190816|BE190816|sn79a08.y1 Gm-cl038 *Glycine max*
BG580331|BG580331|EST482056 GVN *Medicago truncata*
AV423251|AV423251|*Lotus japonicus*
AI896088|AI896088|EST265531 tomato
25 AV413427|AV413427|*Lotus japonicus*
AV426656|AV426656|*Lotus japonicus*
AV416256|AV416256|*Lotus japonicus*
AL385732|CNS0690I|*Medicago truncatula*
AB016877|AB016877|*Arabidopsis thaliana*
30 AV419449|AV419449|*Lotus japonicus*
AI486269|AI486269|EST244590 tomato
AV411690|AV411690|*Lotus japonicus*
AV419925|AV419925|*Lotus japonicus*
AV418222|AV418222|*Lotus japonicus*
35 AV409427|AV409427|*Lotus japonicus*
AC005287|AC005287|*Arabidopsis thaliana*
AV426716|AV426716|*Lotus japonicus*
AV411791|AV411791|*Lotus japonicus*
BG351730|BG351730|131E12 Mature tuber
40 BG046452|BG046452|saa54b12.y1 Gm-cl060 *Glycine max*
AI781777|AI781777|EST262656 tomato

12

- BE451428|BE451428|EST402316 tomato
AI772944|AI772944|EST254044 tomato
AI895510|AI895510|EST264953 tomato
AW030762|AW030762|EST274017 tomato
5 AW218859|AW218859|EST301341 tomato
BE203936|BE203936|EST396612 KVO *Medicago truncata*
AV410289|AV410289|*Lotus japonicus*
AW032019|AW032019|EST275473 tomato
AW030868|AW030868|EST274158 tomato
10 AV421824|AV421824|*Lotus japonicus*
BG646408|BG646408|EST508027 HOGA *Medicago truncata*
AF325013|AF325013|*Arabidopsis thaliana*
AC007234|AC007234|*Arabidopsis thaliana*
AW217237|AW217237|EST295951 tomato
15 AC034257|AC034257|*Arabidopsis thaliana*
AW625608|AW625608|EST319515 tomato
AW031064|AW031064|EST274371 tomato
AF370332|AF370332|*Arabidopsis thaliana*
AB006700|AB006700|*Arabidopsis thaliana*
20 AW035467|AW035467|EST281205 tomato
AL163812|ATF14F18|*Arabidopsis thaliana*
AI896652|AI896652|EST266095 tomato
AI730803|AI730803|BNLGHi7970 Cotton
AW034775|AW034775|EST278811 tomato

25

- The invention provides the insight that RKS proteins or functional equivalents thereof play part in a signaling complex (herein also called the RKS signaling complex)
- 30 comprising molecules of RKS proteins, ELS (Extracellular Like SERK) proteins, NDR/NHL proteins and SBP/SPL (Squamosa Binding Protein) proteins, and the corresponding protein ligands (see for example table 3) whereby each of these proteins interplay or act in such a way that modifying genes, or modifying
- 35 expression of genes, encoding ELS, RKS, NDR/NHL or SBP/SPL, proteins or said ligands may lead to functionally equivalent results (Figure 5. Two-hybrid interaction experiments have for example shown in vitro interaction between RKS 0 and
- 40 NDR0/NHL28 and members of the SBP/SPL family. Here we show that in vivo the individual components of this signaling

complex are regulating identical processes, as based on functional genomics on transgenic plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex. ELS gene products
5 are derived from at least two different genes in the Arabidopsis genome. They show high homology on protein level with the corresponding transmembrane RKS gene products.

However, they lack a transmembrane domain while they do contain a signalling sequence at the N-terminal end. Therefore
10 these proteins are thought to be positioned within vesicles within the plant cell or at the outside of the plasma membrane, within the cell wall of the plant cell. A number of homologues have been detected in other plant species (see list on page 3). ELS proteins are involved in the heterodimerizing
15 complex with the RKS transmembrane receptor at the outer membrane site. ELS molecules are either in competition or collaboration with RKS molecules involved in the high affinity binding of the ligand. The signal transmitted from the ligand onto the RKS proteins is then transporter over the membrane
20 towards the N-terminal site of RKS protein, located on the other site of the membrane. The activation stage of the RKS molecule is changed, as a result of transphosphorylation by dimerizing receptor kinase dimerizing partners. Subsequently the signal is transmitted to other proteins, one family of
25 such proteins is defined as the SBP/SPL family of transcription factors, the other family of proteins is represented by the NDR/NHL members.

The different obvious phenotypes created by modifying the
30 RKS gene products could be effected by one process regulating all different effects in transgenic plants.

All the phenotypes observed can be effected by the process of brassinosteroid perception. In chapter 1, RKS genes
35 are clearly involved in plant size and organ size. Loss of RKS expression results in a dwarf phenotype, similar as observed with brassinosteroid synthesis mutants. It was already known in literature that the phenotypes observed from modifying the

RKS genes are also observed when modifying the brassinosteroid pathway genes and/or their regulation, thereby altering the amount and nature of the brassinosteroids in plants.

Literature which describes the phenotypic effects of modifying
5 the brassinosteroid pathway can, amongst others, be found in:
Plant Journal 26: 573-582 2001; Plant Journal 1996 9(5) 701-
713, genetic evidence for an essential role of
brassinosteroids in plant development; J. Cell Biochem Suppl.
21a 479 (1995) ; Mandava 1988 Plant growth-promoting
10 brassinosteroids, Ann. Rev. Plant. Physiol. Plant Mol. Biol.
39 23-52; Plant Physiol 1994 104: 505-513; Cell 85 (1996) 171-
182; Clouse et al. 1993 J. Plant Growth Regul. 12 61-66;
Clouse and Sasse (1998) Annu. Rev. Plant Physiol. Plant Mol.
Biol 49 427-451; Sasse, Steroidal Plant Hormones. Springer-
15 Verlag Tokyo pp 137-161 (1999).

It is thus believed, without being bound to any theory,
that modification of the RKS genes will result in a
modification of the brassinosteroid pathway, thereby giving
the various phenotypes that are shown below.

20

"Functionally equivalent" as used herein is not only used
to identify the functional equivalence of otherwise not so
homologous genes encoding ELS, RKS, NDR/NHL or SBP/SPL
proteins, but also means an equivalent gene or gene product of
25 genes encoding ELS, RKS, NDR/NHL or SBP/SPL proteins in
Arabidopsis Thaliana, e.g. identifying a homologue found in
nature in other plants or a homologue comprising a deliberate
nucleic acid modification, such as a deletion, truncation,
insertion, or deliberate codon substitution which may be made on
30 the basis of similarity in polarity, charge, solubility,
hydrophobicity, and/or the amphipathic nature of the residues as
long as the biological activity of the polypeptide is retained.
Homology is generally over at least 50% of the full-length of
the relevant sequence shown herein. As is well-understood,
35 homology at the amino acid level is generally in terms of
amino acid similarity or identity. Similarity allows for
"conservative variation", i. e. substitution of one

hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as arginine for lysine, glutamic for aspartic acid, or glutamine for asparagine. Deliberate amino acid substitution may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, and/or the amphipathic nature of the residues as long as the biological activity of the polypeptide is retained. In a preferred embodiment, all percentage homologies referred to herein refer to percentage sequence identity, e.g. percent (%) amino acid sequence identity with respect to a particular reference sequence can be the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, without considering any conservative substitutions as part of the sequence identity. Amino acid similarity or identity can be determined by genetic programs known in the art.

'Plant cell', as used herein, amongst others comprises seeds, suspension cultures, embryos, meristematic regions, callous tissues, protoplasts, leaves, roots, shoots, bulbs, gametophytes, sporophytes, pollen and microspores. A target plant to be modified according to the invention may be selected from any monocotyledonous or dicotyledonous plant species, such as for example ornamental plants, vegetables, arable crops etc. 'Dicotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has two or more free or fused cotyledons. 'Monocotyledoneae' form one of the two divisions of the flowering plants or angiospermae in which the embryo has one cotyledon. 'Angiospermae' or flowering plants are seed plants characterized by flowers as specialized organs of plant reproduction and by carpels covering the ovaries. Also included are gymnospermae. Gymnospermae are seed plants characterized by strobili as specialized organs for plant reproduction and by naked sporophylls bearing the male or female reproductive organs, for example woody plants. 'Ornamental'

plants are plants that are primarily in cultivation for their habitus, special shape, (flower, foliage or otherwise) colour or other characteristics which contribute to human well being indoor as cut flowers or pot plants or outdoors in the man made landscape, for example bulbous plant species like *Tulipa*, *Freesia*, *Narcissus*, *Hyacinthus* etc. 'Vegetables' are plants that are purposely selected or bred for human consumption of foliage, tubers, stems, fruits, flowers or parts of them and that may need an intensive cultivation regime. 'Arable crops' are generally purposely bred or selected for human objectivity's (ranging from direct or indirect consumption, feed or industrial applications such as fibers) for example soybean, sunflower, corn, peanut, maize, wheat, cotton, safflower and rapeseed.

The invention provides a method for modulating a developmental pathway of a plant comprising modifying a gene encoding for a gene product or protein belonging to a developmental cascade or signaling complex comprising modifying at least one gene encoding a gene product belonging to the complex of RKS proteins, ELS proteins, NDR/NHL proteins, SBP/SPL proteins and ligand proteins. In one embodiment, the invention provides a method for modulating or modifying organ size. Plant or plant organ size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex with a method according to the invention is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating

cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth,

5 proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Use of a method according to invention for elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase for example the size of plant

10 organs, the growth rate, the yield of harvested crop, the yield of total plant material or the total plant size. Decreasing the levels of endogenous RKS gene product is provided in order to decrease the size of plant organs, the growth rate, or the total plant size.

15 In another embodiment, the invention relates to cell division. The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery

20 are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides

25 herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and

30 RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKS10 gene or functional equivalent. Herewith the invention provides a method for modulating the number of cells to be formed within an

35 eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes,

especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

5

In a further embodiment, the invention relates to the regeneration of apical meristem. Modification the levels of different RKS and ELS genes within plants allows the initiation and / or outgrowth of apical meristems, resulting in the formation of large numbers of plantlets from a single source. A number of gene products that is able to increase the regeneration potential of plants is known already. Examples of these are KNAT1, cycD3, CUC2 and IPT. Here we show that modulation of the endogenous levels of RKS genes results in the formation of new shoots and plantlets in different plant species like *Nicotiana tabacum* and *Arabidopsis thaliana*. Herewith the invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating apical meristem formation, in particular wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof. A direct application of such a method according to the invention is the stable or transient expression of RKS and ELS genes or gene products in order to initiate vegetative reproduction. Regeneration can be induced after overexpression of for example RKS0 and ELS1; or by co-suppression of for example the endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or co-suppression of these RKS and ELS gene products can be either transient, or stable by integration of the corresponding expression cassettes in the plant genome. A further example of essentially identical functions for for example ELS1 and RKS0 overexpressing plants is for example shown in the detailed description, example 3, where both transgenic constructs are able to induce the

30
35

regeneration capacity of in vitro cultured *Arabidopsis* callus. Another example comprises functional interaction between RKS and SBP proteins which was shown by studies in transgenic tobacco plants in which SBP5 and RKS0 were both overexpressed under the control of an enhanced 35S promoter. At the tip of double overexpressing plants, embryostructures appeared whereas in the SBP5 overexpressing plants alone or the RKS0 overexpressing plants alone no phenotype was detectable at the root tips of transgenic tobacco plants. These results show that both RKS and SBP proteins are involved together in a signaling cascade, resulting in the reprogramming of developmental fate of a determined meristem.

Furthermore, it is herein also shown that several RKS genes are able to regulate proper identity and development of meristems and primordia. The invention for example also relates to fasciation, Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems. A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the responsible RKS encoding DNA sequences under the control of stage or tissue specific

promoters, constitutive promoters or inducible promoters results in plants with localized or constitutive fasciation of stem tissue. Another application is modulating the number of primordia by regulation of the process of fasciation. An
5 example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural architecture of the inflorescence, resulting in a terminal group of flowers
10 resembling the *Umbelliferae* type.

Identical phenotypes can be observed when transgenic plants are produced that contain the NHL10 cDNA under control of an enhanced 35S promoter. The resulting phenotype of the resulting flowers show that flower organ primordia are
15 switched in identity, similar as observed for RKS10 and RKS13. These meristematic identity switches are normally never observed in *Arabidopsis* and the fact that two different classes of genes are able to display the same phenotypes in transgenic plants is a clear indication for a process in which
20 both members of the RKS and the NDR/NHL families are involved. The invention also relates to root development. Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the root apical
25 meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased. Adaptation to soil conditions is possible by regulation of root development of plants. Here we describe several processes in root development
30 that can be manipulated by modification of the levels of RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein
35 belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular

wherein said gene comprises an ELS1, ELS2, RKS1, RKS3, RKS4, RKS6, RKS8 or RKS10 gene or functional equivalent thereof. Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of
5 for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products. Overexpression of for
10 example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between
15 plant and soil. A strong increase of root hair length (elongation) can be obtained by overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant hormones, interaction with
20 the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or ELS gene products. Modulation of the total contact surface between
25 plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the contact surface between plant cells and the soil can be influenced by modulation of the number of root hairs formed or
30 the elongation of the root hairs, as mediated by ELS1 and RKS3.

In a further embodiment, the invention relates to apical meristem identity. All parts of the plant above the ground are generally the result on one apical shoot meristem that has
35 been initiated early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue

and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and / or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering. Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows the formation of completely new types of flowers and fused fruitstructures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly been seen in Figure 29, where RKS10 overexpression results in an extremely bushy phenotype.

In another embodiment, the invention relates to male sterility. Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more introduced gene products interfere with normal pollen initiation and development is therefore highly desired. Especially when the number of revertants (growing normal pollen) is extremely low.

Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment, *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

Furthermore, surprisingly we observe that NDR NHL gene products share homology with the family of syntaxins, involved in vesicle transport, positioning of cell wall formation and cytokinesis.

Table 1

Homology between members of the syntaxin family and the NDR
NHL family

- 5 NHL10= At2g35980
 maaeqplnga fygpsvpppa pkgyyrrghg rgcgccllsl fvkviisliv ilgvaalifw
 livrpraikf hvtdasltrf dhtspdnrlr ynlaltvpvr npnkriglyy drieahayye
 gkrfstittlt pfyqghkntt vltptfqqn lvifnagqsr tlnaerisgv ynieikfrlr
 vrfklgdlkf rrikpkvdcddlrplstsn gttttstvf ikcdfd (SEQ ID NO: 1)
- 10 At1g32270 syntaxin,
 MVRSDNVKFQ VYDAELTHFD LESNNNLQYS LSLNLSIRNS KSSIGIHYDR FEATVYYMNQ
 RLGAVPMPLE YLGSKNTMLL RALFEGQTLV LLKGNERKKF EDDQKTGVYR IDVKLSINFR
 VMVLHLVTWP MKPVVRCHLK IPLALGSSNS TGGHKMLLI GQLVKDTSAN LREASETDHR
 15 RDVAQSKKIA DAKLAKDFA ALKEFQKAQH ITVERETSYI PFDPKGSFSS SEVDIGYDRS
 QEQRVLMESR RQEVLLDNE ISLNEARIEA REQIQEVKH QISEVMEMFK DLAVMVDHQQ
 TIDDIDEKID NLRSAQAQK SHLVKASNTQ GSNSSLLFSC SLLFFFLSG DLCRCVCVGS
 ENPRLNPTRR KAWCEEEDEE QRKKQKKKT MSEKRRREEK KVNKPNGFVF CVLGHK* (SEQ ID NO: 2)
- 20 Below the homology is shown between NHL10 (Upper line) and a
 syntaxin protein. (bottom line). The identical amino acids are
 shown in the middle line.
- 25
 IVRPRAIKFHVTDASLTRFDHTSPDNILRYNLALTVPVRNPNKRIGLYYDRIEHAHAYYEG
 VR KF V DA LT FD S N L Y L L RN IG YDR EA YY
 MVRSDNVKFQVYDAELTHFDLESNN-LQYSLSLNLSIRNSKSSIGIHYDRFEATVYYMN
- 30
 KRFTITLTPFYQGHKNTTVLTPTFQQNLVIFNAGQSRTLNAERISGVYINIEIKFRLRV
 R FY G KNT L F GQ LV GY I K
 QRLGAVPMPLE YLGSKNTMLL RALFEGQTLV LLKGNERKKF EDDQKTGVYRIDVKLSINF
- 35
 RFKLGLDKFRRIKPKVDCDDLRLPLSTSNNGTTT
 R L KP V C L PL T
 RVMVLHLVTWPMKPVVRCH-LKIPLALGSSNST

That syntaxins and NDR/NHL genes share large homology becomes even more clear when performing a database search using the following site:

http://mips.gsf.de/proj/thal/db/search/search_frame.html

5 searching for homologous sequences with the sequence At1g32270

gene code:

predicted function:

	At1g32270 syntaxin, putative	Syntaxin
10	At5g46860 syntaxin related protein	Syntaxin
	AtVam3p (gb AAC49823.1)	
	At4g17730 syntaxin	Syntaxin
	At5g16830 syntaxin homologue	Syntaxin
	At3g11650 unknown protein	Putative syntaxin
15	At2g35460 similar to harpin-induced protein	Putative syntaxin
	At5g06320 harpin-induced protein-like	Putative syntaxin
	At2g35980 similar to harpin-induced protein	Putative syntaxin
	At1g65690 hypothetical protein	NDR HNL
	At4g05220 putative protein	Putative syntaxin
20	At3g05710 putative syntaxin protein	Syntaxin
	AtSNAP33	
	At2g27080 unknown protein	NDR HNL
	At3g52470 putative protein	Putative syntaxin
	At1g61760 hypothetical protein	Putative syntaxin
25	At5g21130 putative protein	NDR HNL
	At3g52400 syntaxin-like protein synt4	Syntaxin
	At2g35960 putative harpin-induced protein	Putative syntaxin
	At5g06330 harpin-induced protein-like	Putative syntaxin
	At5g26980 tSNARE	Syntaxin
30	At5g36970 putative protein	Putative syntaxin
	At3g44220 putative protein	Putative syntaxin
	At3g03800 s-syntaxin-like protein	Syntaxin
	At2g35970 putative harpin-induced protein	Putative syntaxin
	At4g09590 putative protein	Putative syntaxin
35	At4g23930 putative protein	
	At1g61290 similar to syntaxin-related protein	Syntaxin
	At3g11660 unknown protein	Putative syntaxin
	At1g54540 hypothetical protein	Putative syntaxin
	At3g24350 syntaxin-like protein	Syntaxin
40	At5g22200 NDR1/HIN1-like	NDR HNL

	At1g11250 syntaxin-related protein At-SYR1	Syntaxin
	At5g53880	
	At3g11820 putative syntaxin	Syntaxin
	At3g54200	Putative syntaxin
5	At5g05760 t-SNARE SED5	Syntaxin
	At5g53730	Putative syntaxin
	At4g03330 SYR1-like syntaxin 1	Syntaxin
	At3g47910	
	At5g08080 syntaxin-like protein	Syntaxin
10	At5g11890	Putative syntaxin
	At1g17620	Putative syntaxin
	At2g22180	Putative syntaxin
	At5g22870	Putative syntaxin
	At2g46300	Putative syntaxin
15	At2g27260	Putative syntaxin
	At4g01410	Putative syntaxin
	At5g22200	Putative syntaxin
	At4g01110	Putative syntaxin
	At3g52460	Putative syntaxin
20	At3g26350	Putative syntaxin
	At1g08160	Putative syntaxin
	At2g01080	Putative syntaxin
	At5g56050	Putative syntaxin
	At3g20600	Putative syntaxin
25	At3g20590	Putative syntaxin
	At4g39740	Putative syntaxin
	At1g32270	Putative syntaxin
	At1g13050	Putative syntaxin
	At5g45320	Putative syntaxin
30	At3g20610	Putative syntaxin
	At4g26490	Putative syntaxin
	At5g42860	Putative syntaxin
	At1g45688	Putative syntaxin
	At4g26820	Putative syntaxin
35		

40 This observation provides the explanation for understanding
the mechanism by which the RKS / NDR-NHL complex functions.
Cell wall immobilized RKS gene products (containing the

extensin-like extracellular domain) respond to a local ligand signal, in combination with the heterodimerizing ELS protein (s) either as homodimers, as RKS heterodimers or in combination with the heterodimerizing ELS protein(s).

5 Predicted ligands for the RKS / ELS receptor binding consist of peptide ligands (based on the LRR ligand binding domain of this class of receptors). These ligands are normally produced as a pre pro protein. The N-terminal signal sequence is removed by the transport through the Golgi system and
10 allows modification of the ligand at this stage (e.g. glycosylation). The ligands can then be secreted after which further processing is possible (e.c. proteolytic cleavage, removal of sugar groups etc.) The resulting peptide, possible
15 transmembrane receptor complex with high affinity, resulting in transmission of the signal from the ligand through the transmembrane receptor component towards the other site of the membrane.

One class of ligands interacting with the RKS and / or ELS
20 receptors consists of the family of pre(pro)proteins shown hereunder in table 3.

Table 3 Ligands within the RKS signaling complex (herein also called RKS/ELS ligand proteins)

For each ligand (A to N) the genomic structure before splicing and processing 5'- towards 3' is given. Exons are indicated in large letters; introns and surrounding sequences (including leader 5'-and trailer sequences 3'-) are indicated in small letters.
Beneath each DNA sequence the amino acid sequence of the pre-pro-peptide is given. The first line represents the signal sequence
The second (set of) lines represents the pro-peptide.
The last line represents the conserved Cysteine motif.

A. At1g22690

1 attaaacgcc aaacactaca tctgtgtttt cgaacaatat tgcgtctgcg tttccttcat
61 ctatctctct cagtgtcaca atgtctgaac taagagacag ctgtaaacta tcattaagac
121 ataaactacc aaagtatcaa gctaattgtaa aaattactct catttccacg taacaaattg
181 agtttagctta agatattagt gaaactaggt ttgaattttc ttcttcttct tccatgcac
241 ctccgaaaaa agggaaaccaa tcaaaactgt ttgcatatca aactccaaca ctttacagca
301 aatgcaatct ataactctgtg atttatccaa taaaaacctg tgatttatgt ttggctccag
361 cgatgaaagt ctatgcatgt gatctctatc caacatgagt aattgttcag aaaataaaaa
421 gtatgtgaaa tgtatctata taaagaatca tccacaagta ctattttcac acactacttc
481 aaaatcacta ctcaagaaat ATGAAGAAGA TGAATGTGGT GGCTTTTGT ACCTGATCA
541 TCTCTTTTCT TCTGCTTTCT CAGgtaaact gttaaaacca ttttcaagac taccttttct
601 ctattttcaga caaaccaaaag taaaacaatg aaaaatctct ctggctcttc atagGTACTT
661 GCAGAGTTGT CATCATCCAG CAACAATGAA ACTTCCTCTG TTTCTCAGgt aagagtgata
721 caaaaacata ctaaacaaac tttcaagaga gtaatatata aggaaatgtt ggcttctttt
781 ttttgttgct aatcagACGA ATGACGAGAA CCAACTGCG GCGTTTAAGA GAACATACCA
841 CCATCGTCCA AGAATCagtt agtctactct ttcaacactc taattccttt gttctaagta
901 ttttttttgc cccccacaac ctttttttta ttaaatgagc caatttttat agATTGTGGG
961 CATGCATGCG CAAGGAGATG CAGTAAGACA TCGAGGAAGA AAGTTTGTA CAGAGCCTGT
1021 GGAAGTTGTT GTGCCAAGTG TCAGTGTGTG CCGCCGGGAA CCTCCGGCAA CACAGCATCA
1081 TGTCCCTTGT ACGCCAGTAT CCGTACACAT GGCAATAAAC TCAATGTCC TTAAaagact
1141 tctcatttct caactatagt ctcatcttct gattatgttt ctctttttgt tatgttgcat
1201 gtgtgatgtg tgagcttatt attatgttga ttgttgacat aattcaacta tataatttgt
1261 atcgattccg aataataaga tgagtgtatt tattggctat taagtttttt tttttttttt
1321 ttgggcacaa tggctattaa gttttaaaca tctgatttta ttggttacaa aaaaacaaca
1381 agtttcattt tcatattaac acaaaatctc catcacatatt accaaaccaa aaaaatacac
1441 aaggggggaga gagaccaacg gttcttgggt cagagtgttc atcttgtttg agccgtcacc
1501 gtttcttaga ctttaacagcc acaacacctt tataaagctt caccgcatcc ttcaacgcac
1561 ctgcgcgagg ccgagccacc ttattgtttg gatcaacaa caaaacttct tcaaacgcac
1621 tcaatgccaa aggc (SEQ ID NO: 3)

45 MKKMNVFAVFTLIISFLLLSQVLA

ELSSSSNNETSSVSQTNDENQTAAFKRTYHHRPRIN

CGHACARRCSKTSRKKVCHRACGSCCAKQCVPFGTSGNTASCPCYASIRTHGNKLKCP* (SEQ ID NO: 4)

50

B. At1g74670

5 1 gaaaaaaaga agaaaagata atggtccgta ttaatatagt tgaaaacttg aaactacttt
61 ttagtttgta tataatacag tagactaggg atccagttga gtttctttct ttattttgag
121 ttgtgtttta tgtttgattt tacgttttta tatgtaaaata agatatttta cgaattatgg
181 ttttatttgg gtagaagttg tagaatgact taaacaatca agtggcagaa tgagatatat
241 aaagtaatat aatatatgta ccgttatata cttattgtac atgtgaatga ggaagcttac
301 acacacacac cttctataaa tagctgacaa aactgggtgt tacacacaac acattcataa
10 361 atctctcaaa gtaagaacta agagctttac tacagtccta ctctctacac atcttctctc
421 tctctcaaga gtagtcATG GCCAAACTCA TAACTTCTTT TCTCTTACTC ACAATTTTAT
481 TCACCTTCGT TTGTCTCACT ATGTCAAAAG AAGCTGAGTA CCATCCAGAA AGTgtaagtt
541 tttatttttt ggtaaaatag aaagtgttaag ttttataatt cattcaatty tttttgcctt
601 tcccttttcta ttatttgcta taaatctaata acccgcggtta aaattttgttt tgaaattaaa
15 661 cagTATGGAC CAGGAAGTCT GAAATCATA Cgtaagtaaa aacttcttct tcttttatga
721 atcttgtttc ttattatata tcaataaaaa actcgattat catgattgca gAATGTGGAG
781 GACAATGCAC AAGGAGATGT AGCAACACAA AGTATCATAA GCCATGCATG TTCTTCTGCC
841 AAAAGTGTG TGCTAAATGC CTTTGTGTCC CTCCAGGCAC GTACGGCAAC AAACAAGTGT
901 GTCCTTGTTA CAACAACCTGG AAGACTCAAC AAGGTGGACC AAAATGTCCA TAAacaaaaa
20 961 cattgagaga gaaaccccaa tctgtttcct attttattta attatttcca gtagcttttt
1021 gttgtcgtga tggttaaatt atagtgtttt tgcagggtac atttatcatc gataaacaat
1081 atcatataaa atcttctatg tttctttcac gttttgtttc ttttggtgta gtcaatacac
1141 gaaatgtgta tggaccttct aattaggaat atataaaatt ttatttatta attagataat
1201 ctttcgtata gttaaaattc caaggattac ttttgattcg tttgggacaa tctattttat
25 1261 attttacttt ctaagtttgt ataactatat cttaaaagtg ttgacagag tcctaattgat
1321 tttagtataa ttgttactat ttagttacgc ttcgaaaatt tggaaacttt ccaaagtgg
1381 ctatatcaat ttgattcact aatctgcgct tccttctagt tttttacaat tatggagatt
1441 tttcgacgat gat (SEQ ID NO: 5)

30

MAKLITSFLLLTILFTFVCLTMS

KEAEYHPESYGPGSLKSYQ

35

CGGQCTRRCSNTKYHKPCMFQCQKCAKCLCVPPGTYGKNQVCPYNNWKTQQGGPKCP * (SEQ ID NO: 6)

C. At1g75750

5 1 cacaactttt atacgcacca ccaaccgacc cattttgaaa aagagaaaat aaaccacaaa
61 aacacacata aataatatgc tgataacaat gtcttaaaaa tctatttacc atttctagta
121 atcaatatct attgcaaaaa atatttataa gaatacaaat gaaaaatgat aaaatacaaa
181 tgattttctca attacctaata aaatataaaa atgtcttact ttattttcag ccactgttgg
241 aaagtacttg caatcataatc gtattttgaa ttataaaaact cagaaacaat tattttccct
301 gaaaagttta aacttttaat aagatattta taaaataaaa agaatagtct agaccgaaaa
10 361 tgggggtcggg tgtccatcca aaggagtgcg ataaatagaa ccctccaagt tctcattagg
421 acacaacaac taaaaccaca tttatcatta cagtctgatt tgagctaagt tctctcatca
481 taaactcttc ttggagaatc ATGGCTATT CAAAAGCTCT TATCGCTTCT CTTCTCATAT
541 CTCTTCTTGT TCTCCAATC GTCCAGGCTG ATGTCgtacg tctttttcat cacaactaa
601 ttataactca tataataactt atgttttcaa aaacatattt ctcacatgtt acaacaatat
15 661 tcttgagga AAACTCACAG AAGAAAAATG GTTACGCAAA GAAGATCGgt aattatatga
721 tttttattaa acctaacggt aaatttagag tgagattaat aatctgtgtt tttctttctt
781 gtatatatag ATTGTGGGAG TGGTGTGTGA GCACGGTGCA GGCTTTCGAG GAGGCCGAGG
841 CTGTGTCA CA GAGCGTGGG GACTTGTGC TACAGGTGCA ACTGTGTGCC TCCGGGTACG
901 TACGGAACT ACGACAAGTG CCAGTGCTAC GCTAGCCTCA CCACCCACGG TGGACGCCGC
20 961 AAGTGCCCAT AAgagaac aaagctctta attgtgcgg ataatgggac gatgtcgttt
1021 tgtagtatt tactttgcyg tatatatgtg gatcgaataa taaacgagaa cgtacgttgt
1081 cgttgtagt gtgagtactg tattattaat ggttctattt gtttttactt gcaagttttc
1141 ttgttttgaa tttgtttttt tcatatttgt atatcgattc gtgcattatt gtattatttc
1201 aatttgtaat aagattatgt tacttttgag tgggtgttta tcatactttt tttctatggt
25 1261 aagaggtttt ggaaaagtat cgagaatgat atataaagta attttgatat cgacgcaaga
1321 tgataactac tagactagct gagtataaga atattgatgt atatatttgc ggacaatttt
1381 gaatttatta taccattatt taatcacgac catataaaaa taattcttgt ttgcgttata
1441 atttgtgtta atacgataga gtagacaaat ga (SEQ ID NO: 7)

30

MAISKALIASLLISLLVLQIVQA

DVENSQKKNGYAKKID

35

CGSACVARCRLSRRPRLCHRACGTCCYRCNCVPPGTYGNYDKCQCYASLTHGGRKCP* (SEQ ID NO: 8)

D. At2g14900

5 1 ataactaaca atggttgagt ggagatgtgc ttttagtcaa gtggttaaat atatttgact
61 tctgtttttt cattggagtt tgactctact aagttgtgtt tcctcgcgta gtaagaattg
121 gttatggatt agaccgtatc gatctaaaga tgtcaaagaa aaaaaaatgt ggttgtgtaa
181 agtaaatatg tagattgtgg cggattaaag tatgttttga ttcacatcat tattgttatt
241 ttttcatgaa ttctaaatgt aaagttctta taatcttatg ttacttttta caaattgtaa
301 ggattactct gaaatttgyt atcgaattct aagacaaata caaataaaca atgactgaac
10 361 aagttgataa aacataatgg aaggaataat actgcagttc tattaataac taaagaagtt
421 ggtagattgg cctataaaag gagaataaag agaccacaag aaggtctatt attcggggac
481 taaagaaagc caaagaaaac ATGAAATAA TAGTCTCCAT CTTAGTGTTA GCCTCTCTTC
541 TTCTAATCAG TTCATCTCTT GCTTCGGCTA CTATATCAGg ttggttctaa tctcttcaag
15 601 aatcttcttc tctctatttt ttttttcttc ataaagttag ttatgttatg attggtttag
661 gtcacaattg tttctttatg ctttcgtttc cataagaaaa atattacaaa tatttaactag
721 aacaacataa catgcaaacg agtaatacaa aattcattat tatgatcaaa acaatcatga
781 attagttgga cttatttgtt aaattccgaa aatctcacta aaataaagtg aacttcatct
841 acatggcttt agacgcaaaa tctttaaggy tatctacaca agtttggaat gaataatttc
901 ttgcgatggg agtgtagaag gatctagaag atccacaaga tcattagtgt atcttctaga
20 961 tctttttaca ttgagaagtg aggagatatt tgttgtatta gaaagaatta tagtgaagta
1021 aattttttta ctatgtacga tcattttat acgatacttt tattaaggat cttgtggatc
1081 ttctagATGC TTTTGGTAGT GCGCGGTAG CTCCGCGACC GCAGAGCAAA GATGGACCGG
1141 CGTTAGAGAA ATGGTGTGGA CAGAAATGTG AAGGGAGATG CAAAGAAGCG GGGATGAAAG
1201 ATCGGTGTTT GAAGTATTGT GGGATATGTT GCAAAGACTG TCAGTGTGTT CCTTCAGGCA
25 1261 CTTATGGGAA TAAGCATGAA TGTGCTTGCT ATCGTGACAA GCTCAGTAGC AAAGGCACCTC
1321 CTAAATGTCC TTGAttctat ttctttccaa ccaaaaattt aaataaatga ataagagaga
1381 tccagtaaac taataataaa ctataaatgg atcttttgtt tatgattttt tttttttcat
1441 ttctattttt acgaatttgt cttggtcttt ttgaagtaag tttttaaata ttgaaaagtg
1501 ctaaaattat gtggaatcg ataagttaa tgaatgatat aatatataag tcttcagttt
30 1561 ttgtaagaaa cttgaatata aataatatt catcaaacat aataataaaa tatattgtat
1621 aattagattg gctcaaccga tataaacaat tgaatcgaat tttttcttct aaatatitaa
1681 tcatccaaat ttgtattgta ccaatgaatg agatggttat gaggactaga agatagagag
1741 gagaagaacg tgtttggtaa aataattatg atggagttga gacaactttt aagagatttt
1801 aaaaagactg actaacgtgt taggttcac acgt (SEQ ID NO: 9)

35

MKIIVSILVLASLLLISSSLASATIS**DAFGSGAVAPAPQSKDGPALKW**

40

CGQKCEGRCKEAGMKDRCLKYCGICKDCQCVPSGTYGNKHECACYRDKLSSKGTPKCP* (SEQ ID NO: 10)

E. At2g18420

5 1 gccaatgggt aactgaggaa gaaggataag accaaaaaaa aaactaaaat ggacagattg
61 aattagtaaa aagataaatt ctaaaaaccg aaacaaatct taagttgggt tatacacatc
121 tgcattgacc aacaaaagaa agtagactga aatttatttg aaaatgatct tgtaaaaggca
181 tattatataat ttaatttagg aaatgaatgt taaatccttt aaattgtttt gatttcacaa
241 aaggataaag aaatattggt tacatacatc ttaatgtgtt gacccaaaaca aataaaatgt
10 301 gataagaaac aataaaacca ttttgaccaa agttcttata gttttaatat tctttaattg
361 tcatttggta gtgactaata atattacatt aaacctaatg tataaataga agcccatct
421 tctacgcctt tataattagc aacaaccaaa aacattcatt tgtcattttg tctcctcttt
481 tgttttctct gatcactagt ATGGCTGTAT TCAGAGTCTT GCTTGCTTCT CTTCTCATAT
541 CTCCTCTTGT CCTCGACTTC GTCCATGCCG ATATGGTGgt acaattttaa caaccaaata
15 601 tattttctta tttgatttta ttttttcaca acttttgtct acgttctaata ggaatttttt
661 tcaaaatatt catgcagACG TCGAATGACG CCCCTAAAT CGgtaatatc tctatcatat
721 aaacacgtac gttgaatttc tatatacgtg tgtttaattg aagttttggt tggaaattgt
781 atgtatttgt agattgcaac agcaggtgcc aagagCGGTG CAGTCTTTCG AGTAGGCCAA
841 ATCTTTGTCA CAGAGCGTGC GGGACTTGCT GCGCTAGGTG CAACTGCGTG GCACCGGGCA
20 901 CATCCGGAAA CTACGACAAA TGTCCTGTCT ATGCTAGCCT AACCACCCAC GGAGGACGCA
961 GAAAGTGTCC Ttaaaaactc tgtcgtctgt tgatttgatt tctgtttataa tactttactt
1021 ttatgagagt aatttgggtt attttcttgg gaattattaa aaagcaaaag aaagagaatg
1081 ttatacgtca tgtgcaactc ttcgatcttt gtttagtgt ttatccaatt tgtacttggt
1141 ggtttgggtc ctgggttaaca ttaggcttga aaaggtattg ttttctatta tacaattcac
1201 taaataggca tcytacttgc atataaaata aagaatgaag agagaagtaa aagagttttc
25 1261 tttttttact catggaagt aggcaatggg tttaaataag gtaacaacag aattggaggg
1321 gacttaatga actatgacgt aaaactgaga gcyattgaat atgtaacgtt accaacaata
1381 ccaataaaat tatgaagat agtatatgaa attacgttta attaatgttt ccgggttgaa
1441 tgtattatat atagaagtaa cagtacgatt ttattacat ttttgtaaa gattcctaga
30 1501 aaggataaac ctctataaag ttaataatag tcttgagtct tgactcttcg aggcataata
1561 attcacgcga taattaatcg ttcaactatt attctatatt ctatataaca tgagcttcaa
1621 caaaagaagc atcaatcata tcttcaacag tatactgcag tgtaatgtaa catattcaag
1681 atcaaacggg acaaaaaagc aagataccgt cgaaacaatc aaaccccatg tatcataaac
1741 tcccatcttc tctttcctaa attccccgtc gcttgacaaa tc (SEQ ID NO: 11)

35 MAVFRVLLASLLISLLVLDFVHA

DMVTSNDAPKID

40 CNSRCQERCSSLSSRPNLCHRACGTCCARCNCVAPGTSIGNYDKPCYGLTTHGGRKCP* (SEQ ID NO: 12)

F. At2g30810

5 1 cttttatttg tttgtgaaaa aaaacaatag cttttatttg tcctaggaat tatttaatag
61 attaaataac agctattttt ctcttatttc ttagtgatta aaatatttaa aatacagacc
121 aaaatttaatt gtttatgtta atatatttac tcctlaatcc ttatatatta aattgtataa
181 tgcattgtagt taataaattg ttttccaaaa ttcattcata attttatttc taaattattt
241 tggtaagaa aacacatctt tgaataatta aatgcttcct tgtatttgat aatttcttga
10 301 tattttaaaa taccttctat actatgccaa tgttattggt tataaatagg tttaacattg
361 atcctgaaat atatcataag aaaatcaaaa gtgaaataag agatcaaaAT GATGAAGCTC
421 ATAGTTGTCT TTGTTATATC CAGTTTGTG TTTGCTACTC AATTTTCTAA Tgtaaaaatt
481 attattattt tcttcattat atgatttatg aattcagaga aataaagttt ttttttttat
541 gtgtgtatgt acagGGTGAT GAATTAGAGA GTCAAGCTCA AGCACCTGCA ATCCATAAGg
15 601 tatattttaa ttataaaata tcaataactg aataataaat aataaatata ttacaacaag
661 aatatcaatg ttatttttca aactacataa ttttaaaata ttttattgat aacacaaatg
721 tatattatta tcgtctccat tgatttgcac tctaaatttg tttttgttat ccaaccaatt
781 tcagAATGGA GGAGAAGGCT CACTTAAACC AGAAGgtaaa ttgtttaaaa gatattattt
841 ttattttatat agtaaatgat tgatcaaatc acaacttaaa taatttaatt gttgatttat
20 901 atttttctga agAATGTCCA AAGGCATGTG AATATCGATG TTCGGCGACA TCTCACAGGA
961 AACCATGTTT GTTTTTTGC AACAAATGTT GTAACAAATG TTTGTGTGTA CCATCGGGAA
1021 CATATGGACA CAAAGAAGAA TGTCTTGCT ACAATAATTG GACGACCPAA GAAGGTGGAC
1081 CAAAATGTCC ATGAAAACAA aaaattgtaa aagcaaaata aaatctatcg ttgttatctc
1141 tcaataaaat ctatgtttgt aatccttggt tttcaatata gaatataata tggagttttc
1201 ataatttctt ctattacaaa attaaagtta atgcacaaat aaattgaagg gacttggacc
25 1261 ttttcgtgta agttctttct ttaaatcacg aacaatttag atttatattt tcaactctac
1321 aaacacaaaa catggatgct ctttaactct catccaaaca aaatgcattt ctctctttct
1381 ttttctaaac atttcacaac aatatcccat attatatcta agatatatga tctttttaa
1441 ttgaatttat ttaggccatg ttttaaaatc gtgtttggtt agattgacct atgaaatggt
30 1501 gacatatttt aacattccta aatatgacta aaaatgatta aagatattha ataatatatt
1561 tgctctatta aaaatgatta aataaataat aata (SEQ ID NO: 13)

MMKLIVVFVISSLLFATQFSNG

35

DELESQAQAPAIHKNGGEGSLKPEE

CPKACEYRCSATSHRKPCLFNCNKKCNKLCVPSGTYGHKEECPCYNNWTTKEGGPKCP* (SEQ ID NO: 14)

40

G. At2g39540

1 taatgctata cttttaatct ataatatata ttagatgtga ctttaaggaat ttcaatagtt
5 61 atacataata ataaaaatga atatttggtta gtgttacaaa ctgtgtgtca taatcatcat
121 tcatcaggat ttcaaaaata tctcaaaatt gttgtaagtt catgtaattc gaaatgaatg
181 tgcactataa gaaataaatt tacaatttaa aaaatgcttc aatactggtt acaaaaaaaaa
241 ctttcaatac tagtattata ctacttactt agtcaaaaaa gtttatgaat atgggttttt
301 ctgtatgtta atatttttaa ctgaaaatag taccgacata acaagtaaag atatctttat
361 ttaaagtaac aaacattaat ttcaacttcaa attctcacta ttaaggattc ctctctttgt
10 421 agccacattt caccatcact actttgtttt cgcatacttt taaattttgt atacgtagca
481 aactctttcg agaaaacaag ATGAAGCTCG TGGTTGTACA ATTCTTCATA ATCTCTCTTC
541 TCCTCACATC TCAATTTTCT GTACTTTCAA GTGCTGATTC GTgtaagtg ttacttaatc
601 tagttaataa ttgtaggtca tgcattgtatc attttgaac aagttttctg aaatttctaag
661 attttacata tatatgtgat aaatgaatta gcagCATGCG GTGGAAAGTG CAATGTGAGA
15 721 TGCTCAAAG CAGGACAACA TGAAGAATGC CTCAGTACT GCAATATATG TTGCCAGAAG
781 TGTAAATTGTG TTCCTTCGGG AACTTTTGA CACAAAGATG AATGTCCTTG CTACCGTGAT
841 ATGAAAAACT CCAAAGGTGG ATCCAAGTGT CCTTGAacgt tctttgaaga tcctcatcac
901 atacataata cttctacgta ctatatgtgt ggaaatatta atcacattct atgtttgaaa
961 tatataaaat aaaatcaatg cccccaatgt tggaaatctt caatgtgata tcttaataa
20 1021 tatcacgaat aaaaaagttt aaattttctca atctcathtt taatctttta tctaatttct
1081 taacacatca acgaatcttt aatctttaat catgtagata attatcagag cacctaaaca
1141 ttgcgcggtt ttgtgattat acaaagtaac atcgtgctgt ttttgacttt tgaaaaccac
1201 agatccaaaa actgtttact ttctcttaag agaaagcaaa gccgagttag tccaagcgag
1261 ttttgagaga ttctgttact cactaccgga gaacgacgct atgtcagaga ccgccgtgtc
25 1321 aatcgattcg gaccgatcta agtcggagga agaagacgaa gaagagtatt ctccac (SEQ ID NO: 15)

MKLVVVQFFIISLLLTSSFSVLSSA

30

DSS**CGGKCNVRCSKAGQHEECLKYCNICQKNCVPSGTFGHKDECPCYRDMKNSKGGSKCP*** (SEQ ID NO: 16)

35

H. At3g02885 (GASA5)

5 1 cgctttctat tacacttttt tttcttttta gtcgcacttc acaattagct taattaattt
61 cctaaactcg cttattttcc cctttctata tacagatatt atcatttagtg acattttcat
121 tttccaaaca gagcgtttag acactagtca actacacaat ataattttcc aattttcact
181 gagagaaatg tttttttttt ttttttccaa ggcaagattt tagtcttttg gttctctata
241 cytgggtaat tagtgattga taatttacac tgttgagtct ttgacattgt ctaagagaca
10 301 aaaacgacaa gtgtggtacg taattagaaa ttaaaatgac ctacttcccc agaatacag
361 catgaacatt ggcaatacca aatttcttga ataccattga aggaatcca cactaatcat
421 tttctctata aatatcttta atccgtttta ttgtttctta agaatcatte attggcaatc
481 aagatttttt aacaaaaaaa ATGGCGAATT GTATCAGAAG AAATGCTCTT TTCTTCTTGA
541 CTCCTCTCTT TTTATTGTCA GTCTCCAACC TCGTTCAGgt aaaccactca aaacagattc
15 601 agtttatata agtctgatat tgaagtttta tatattacag gctgctcgtg gaggtaaaaa
661 tgaccaaaagg ctatacattc cttaaaaatt taatggctat tagttttctg atattgaagt
721 tttatatata tatgacagGC TGCTCGTGGT GGTGGCAAAC TCAAACCCCA ACgtacggac
781 tcaaaacttt tgttgtttca tatgatcata ttaatttatt aatcactaat tattgataat
841 gttgataaat aaactttaaa gtaacaataa tgggttttat tttgtgaaat gtcagttttc
20 901 tagtatactg tatgctgtga attataagca tgaacataaa gatctcaatg atttgttttt
961 tgtttgtttg ttgtgatatg cttttttgat ggaacttca attgtagAGT GCAACTCAAA
1021 GTGTAGCTTC CGTTGTTTCA CAACATCACA CAAGAAGCCA TGCA TGTTCT TTTGCCTCAA
1081 GTGTTGCAAA AAATGCTTTT GTGTTCTTCC TGGCACTTTC GGCAACAAAC AAAC TTGTCC
1141 ATGTTACAAC AACTGGAAGA CTAAAGAAGG CCGTCCAAAA TGTCCTTAAA acttcttttt
25 1201 agatataatt gataatattc atctagtttt ggattatcaa acacttacta ctctgtttta
1261 atctgtttct acaagttggc gatttgtctc tacacttttt ttgtgtcttt tgctcttaac
1321 tgttgtgttt gttatacgtg taagcccgcc caatgtgtca tggccgaact tattatgggt
1381 acatatttat gaaatgggct tcattatcaa ttgatttgag cctacaaaaa tgtagccata
1441 aagcccatga agttgtaatt gttaatatat cagtcataaa tatgattttc tatatctatg
30 1501 atttatctct agtgttgatg atgtttgtat gtggaagtca tgttctattt gcttccacgg
1561 tttaaaaacc atcaacttgc taaggtcaaa ttctaataat actgtgaaaa acattattta
1621 cgtgcgtaat tatatgaatt tatgaatagg ttttaattcc attttttcct aatagtgttt
1681 tatgtcaaa (SEQ ID NO: 17)

35

MANCIRRNALFFLTLLFLLSVSNLVQAA

40 RGGGKLPQQ

CNSKCSFRCSATSHKKPCMFCLKCKKCLCVPPGTFGNKQTCPCYNNWKTKEGRPKCP* (SEQ ID NO: 18)

45

I. At4g09600 (GASA3)

1 taggctggca atttaactct gagacgtctt tcttgatat agaataaaac atacgcgtgt
5 61 aaaagaaaac gcgatgaatcg aatgatgagt gttaacgttc gatcgagatg ccaccaaatc
121 ttttcattaa aatgaattgt ggaggacata ccacttttaa cgagggtcatt tccactgggt
181 gacatgtgga ctctactttg ggtggcatgt tcatactctt ccacatcacc atgtaaacgt
241 gaaaacaccc accacactca cttacatctc aaacacatgt cttcattatc gtacgtagct
301 ccaaaaaaaa aaatgaaaac taggtttagt gattctatct cgcaatgtat aatatacaac
10 361 ttgtaaaaat aaaatatttg aataagcatt ataaataaac ccaaagaggt gttagattta
421 tatacttaat tgtagctact aaatagagaa tcagagagaa tagttttata tcttgacaga
481 aactgcatgc tttttgagac ATGGCAATCT TCCGAAGTAC ACTAGTTTAA CTGCTGATCC
541 TCTTCTGCCT CACCACCTTT GAGgttcata acttttgtct ttacttctcc atgaatcatt
601 tgcttcgtct tatccttaat tcatatgtgt ttgatcaatg ataataatc atcattctct
15 661 tcagCTTCAT GTTCATGCTG CTGAAGATTC ACAAGTCGGT GAAGGCGTAG TGA AAAATTGg
721 tatgtaacgc taacatatat gtaaagtgtt atactctgtt ttatatatga tttttaaacg
781 gttaaaaact agtcataatgt gtataaatat atcatgtgaa gATTGCGGTG GGAGATGCAA
841 AGGTAGATGC AGCAAATCGT CGAGGCCAAA TCTGTGTTTG AGAGCATGCA ACAGCTGTTG
901 TTACCGCTGC AACTGTGTGC CACCAGGCAC CGCCGGGAAC CACCACCTTT GTCCTTGCTA
20 961 CGCCTCCATT ACCACTCGTG GTGGCCGTCT CAAGTGCCCT TAAacatata cacatacaga
1021 tgtgtgtata tgtcttccgc gagcacacac gtacgtttat gttttaagga caatagtatg
1081 tatgagcagc tataaacaaa ccagaagtta atggttcatg ttgaactagt ataagttgta
1141 tgaactgtgc tttttttgaa caaccacttt tgctgtaagt ttagcaaccc tatttaataa
1201 attagagatt acaaaaaaaa aaatgaaaaa tgtttaaaaa acgtggattt ttaaatattg
25 1261 gattaaaaat taattttcat tttggttgat ttgtcaataa attagctaag ttttgtatac
1321 taggccgttt aagatatgct gttaaatttt tgataataga gttgccttag aagttcataa
1381 ctgtaaatat ctaacttcac ttcaatctca caaacacacg aatcaacttc agcactaaga
1441 atcgaattga ccagaactga aagaaagtaa aagaaaagct gaatacagag aatttaacga (SEQ ID NO: 19)

30 MAIFRSTLVLLLILFCLTTF
ELHVHAAEDSQVGEVVKID

35 CGGRCKGRCSKSSRPNLCLIRACNSCCYRCNCVPPGTAGNHHLCPCYASITTRGGRLKCP* (SEQ ID NO: 20)

J. At4g09610 (GASA2)

5 1 ttaacagttt aacaccataa tgttaaactc ggtttagcat tttggtgtaa ttctacctct
61 ttaaccatac atactaaaga cgcagagaag ttcatatggt agttaatcgt aaatagctaa
121 actttttaatt gggggttaaca tattatttaa cacttaacat ttaactattg atctctcatt
181 ttttttttat taacccaaat aaattcattt tagaaccaaa cgtttcaaaa actcgtaatg
241 ttttctcatt aaatcttatac tatagctcac acaaagaaaa actacggaca tgcattgacc
10 301 caattatata catggattat tatttttagt gttataatat gatacaaaat aaaaaacatt
361 tggatagccg ataggcgata gccactataa atataccaaa gaggttggat tatacatata
421 gccgtaatac caaagagagt atcagataga aatagttcta atattttgta caactcacag
481 aaattgcatg agtttcgaac ATGGCAGTCT TCCGAAGTAC ACTGGTTCTG TTAATAATCA
541 TCGTCTGTCT CACCACTTAT GAGgtttata atatttttgg tctttatagt tccccaagaa
15 601 caccatagcaa tattatactc aattcatgtt tatatgataa tgactgatca ttctcttcag
661 CTTACAGTCC ACGCTGCTGA TGGTGCAAAAG GTCGGTGAAG GCGTAGTGAA AATCGgtatg
721 taaccctaac ttatatataa cacgttggta tataacttaa tatttctgat ggggtgcactc
781 tcttcccaac ttatatatat ctttgttatg gagaatgtct caagctttta atgagatgtt
841 atatctcgga gaaggaaact atgaactaaa agctttggat tcctttgcaa caaatataaa
20 901 cttttgatgg gtttaaacgg attaaattag ttacatgtgt ttgatgaatg tatgtatgat
961 tgtagATTGT GGTGGGAGAT GCAAGATAG ATGCAGCAA TCTTCGAGAA CGAAGCTATG
1021 CTTGAGAGCG TGCAACAGCT GTTGTTCCTG CTGCAACTGT GTGCCACCTG GTACTTCTGG
1081 AAACACCCAC CTTTGTCTT GCTACGCCCTC CATTACCACT CACGGTGGCC GCCTCAAGTG
1141 CCCTTAAaat ttcttctgtg tctgtttctg tttctacttc tatttcgaat atatgtacat
1201 gtgtgtgtac gtgtgtatgt atacaagtac tgctatgttt tggaggacaa aagtatatgt
25 1261 atgagaagct ataaactaat tagaagtga tggttatgag tattatcaaa ccgtgttact
1321 tctgaacaac caatttcggg ttgttccaag tttggcaacc ctaaaataaa aattcaaaat
1381 gattggagac tactcgttta tagacattga aaacgatgaa atctcgttac gtttttatat
1441 tttttgaact gtaattatat tatgcagaag cggttttcta atgggcccac aaaaaaaaag
30 1501 tggttttgta atggatatga ttcggatcta ttctggaaat ggtctcaaaa agtagagttg
1561 agatctcaat acgaaaatga accctttcgt ttgatttatc aaagcctttt attttgaaaa
1621 cgttaaatcc tcactaggat ctctctt (SEQ ID NO: 21)

35 MAVFRSTLVLLIIVCLTTY

ELHVHAADGAKVGEVVKID

40 CGGRCKDRCSKSSRTKLCLRACNSCCSRCNCVPPGTSGNTHLCPCYASITTHGGRLKCP** (SEQ ID NO: 22)

K. At5g15230 (GASA4)

1 aaatattcac cctaaaaatga atctaaaaat gtacaaaatc acaggaaaaat aaaactaagc
5 61 agaaatgtcc taagaaaact aaagttttta aaaaataatc ttcaaagaga tactccaact
121 ggtgttataa gcaaaacttg atttatcaaa aacaggttca tagtatttta tatttagtac
181 tataagcttt ccttaaacca tgtgcaaaac catctaccgc agtctaatta ccaatagcaa
241 gtaataaaat gggactaaca ttggaggcat acgtggaata atataattgg aggaatacag
301 taataatgat atgtgtttgcc acaggggaata attgatacga gcaaatygt gtatatatag
10 361 cttatatgca acatcattgg gtcctcaacc aaaaactcct ctctcagtac acttcttttc
421 atacctcaag agactaaaac tagtttgagg agatttagag gagtgtttgg ttctttggat
481 aacaatatcc caaactgaaa ATGGCTAAGT CATATGGAGC TATCTTCCTC TTGACCCCTCA
541 TTGTCTCTT CATGCTTCAA ACCATGgtaa cacctctatt atttttttct tctttcaatg
601 tttgaaaata ttgaagataa tatatttgat tgttttcctt attgacgaac gatatgagac
15 661 aaatgtgggt tctattattg tacttttagt tggaaatata ttaatttagc ctttttaatg
721 aaattaattt tacttgtttt tcctctctct ttttttcggt ttttagGTTA TGGCCTCAAG
781 TGGATCTAAT GTGAAGTGA GCCAGgtcag ttttattatt gaatcgacta gtaattacct
841 tctaaactat attttatacc tattgttatc tcgtaactta acgaaaagtg attaatatg
901 tacttttttt ggttaatttt cagAACGTT ATGGACCAGG AAGCCTGAAA CGTACCCgta
20 961 agttttttct tcacagctat tcttaacaa ttttttttta atctcataat cgacgaaaaa
1021 taacaatttc aagaaatcct ttatttgttt ataataaaaa aaaataagca tttcagttgc
1081 agaaaaaag ttgaaagtga agtgtaagt ggactgtttg gtcagatccg tagactcaaa
1141 atatattaga tattgacgaa attgcccctt aatatgggtc tacagtcaaa gcaaccact
1201 atcttgagac ccacaaaaa gtaaaaaaaa aagctaata atttccacta gattctgttg
25 1261 tttttattag taataaaaaa tttttgagtg ttaacatttt gatattgttt gtatttga
1321 caaccagAAT GCCATCGGA ATGTGATAGG AGGTGTA AAA AGACACAGTA CCACAAGGCT
1381 TGCATTACGT TCTGCAACAA ATGCTGCAGG AAGTGCTCT GTGTGCCTCC GGGTTACTAT
1441 GGAACAAAC AAGTTGCTC CTGCTACAAC AACTGGA AAA CTCAGAGGG TGGACCAAAA
1501 TGGCCTTGAA aaaatctccc ttctgtccct ttttataata aaaattttca actataacta
30 1561 aatttccttt gatcaatggt ttatctactt tattcctaatt gttgtaatgt tatgtcactc
1621 cttttcggat ttgtttctaa atcctaaaaa aaatgagagt ggccttatga atgatatttt
1681 tcatgaatac ttgtgtttct aaagataatt tccattcat ccacaaaaa aaaagatatt
1741 ttccatttcg aaaatagtaa tactataaag gtaaggcaa accaaataat acaatttaaa
1801 aaattcctgc gaaagaagta tgcataatga gaaaagagt acattgggtc tctcgccca
35 1861 gtactaaaaa gccattatt gatttttcca agctttttac aaaatcacgt gttctaacgc
1921 gattgctttt tgcgcaatc ttcttttata caagacttgg gctttgggca gttggaata
1981 aataacgaca acgatatttt acaatcgggt (SEQ ID NO: 23)

MAKSYGAIFLLFLVLFMLQTMV

40

MASSGSNVKWSQKRYGPGSLKRTQ

CPSECRRCKKTQYHKACITFCNKCCRKCLCVPPGYGNKQVCSCYNNWKTQEGGPKCP** (SEQ ID NO: 24)

45

L. At5g14920

5 1 ttgctcaactg gtgcaataat cgaagtgaag agcctcttta tatgaaatat ataagcgaca
61 cagcccttatg ggcaaatcga atgctattta tttatttgat aagaagatta ataatttcaa
121 tttgtcatcc actagtctct tggggtactc aaaacatata accaaaaagt ccatagagtt
181 atttgttctt atttactgat aaagtattcc aagttgatgt acgaataaag tggcaatttc
241 atgtattatc aatataatcc atttttggga atctgatatt ttgtttatcc tcgagctctg
301 agagatatat tttggtgcag tgaaggttca aagctggcat gcatgatgca tataataact
10 361 gctctggacc taatacttac tacgcattta aattaatatt tatggataat atggttaata
421 aataaggaac ttctatttat atcacaaaag gtcactggtc ttcttcgtgt gacttcacca
481 ctttctcatc tcccacaaaa ATGGCTCTCT CACTCTTTC AGTCTTTATC TTTTCCATG
541 TCTTTACCAA Tgtaagttaa tcttactttt cataacaaaa ggtgttatta tgttaaagac
601 tacataatag tatacaatta tgtgcattac gttttcgcgt attgtaacta actatgtatt
15 661 ttgatttaac accgagcagG TTGTTTTTGC TGCTTCAAAT GAGGAATCCA ACGCCTTAGt
721 acgttttcta atttccagtt taattatttc tatgcgtctt taactatata ctccaggcatt
781 tttattgatt attgtgtatg aagttaaatt ttggtatatg ttgtattaa atttatagGT
841 TTCTTTACCA ACGCCAACAC TTCCATCGCC ATCTCCGGCT ACCAAACCGC CGTCGCCAGC
901 TCTCAAACCG CCGACGCCGT CGTACAAGCC ACCCAGCGTG CCAACTACTC CTATTAAACC
20 961 ACCCAACCA AAACTCCGG TCAAACCTCC AACTATTCCG GTTACACCAG TAAAACCTCC
1021 GGTFTTCAAT CCTCCGATCA AACTACCGCC GGTACAACCA CCTACGTACA AACCCCCAAC
1081 GCCAACAGTT AAACCACCGT CCGTCCAACC ACCTACGTAC AAACCCCAA CTCCAACGGT
1141 TAAACCAACC ACTACATCAC CGGTAAACCC ACCCACTACG CCACCAAGTC AATCACCGCC
1201 GGTCCAACCA CCTACGTACA AACCCCAAC GTCACCGGTT AAACCAACCA CCACAACCTC
25 1261 ACCGGTTAAA CCCCCACCA CGACGCCACC GGTCCAACCA CCTACGTACA ATCCCCAAC
1321 TACACCGGTT AAACCACTA CAGCGCCGCC TGTCAAACCT CCAACACCAC CTCCCGTAAG
1381 AACTCGGATA Ggtaataata attttcttcc aaaagtgtga tgattatcgg tcgttgatta
1441 gatcggatgt ataattggac taaatttttg acggtttaga TTGCGTGCCT TTATGTGGGA
1501 CGAGGTGTGG GCAACACTCG AGGAAGAAGC TATGTATGAG AGCGTGCCTC ACGTGTCTGT
30 1561 ACCGTGCAA GTGTGTCCC CCAGGCACCT ACGGTATATA GGAGAAGTGT GGATCTTGT
1621 ACGCCAACAT GAAGACACGT GGTGGAAAT CCAATGTCC TTGAacctt atatgacgat
1681 ggttggttaa cgaataaatt taaatcaatg gagtttttat aagtttgtaa tgcgtttgtt
1741 ttgtttatag taatattgag ttggatcttt gttacggga cgtagaatac taaataatga
1801 aaaaaacctt ctgatgaat taagggtttt atgaatttgt ttgtattga ataataatag
35 1861 gatggataaa gttttattat tctaacaggt tactttatta ggcatttctt cggctcatgt
1921 aactcttgta tcgctgaaac tatgtaatag atagaagaac ctaaaaaag aaagaaaaca
1981 agaaatgcac atagcgaagc tcaaaagatg agtgttctgc tagcggtaat gttgttattc
2041 agttgggtca aatgctctaa ttgcaaatct tatttgggcc ttatatagac tcttatgtgc
40 2101 atatggtcca gcctatttg gccgatgtgt ttgaagatca tttgggaaag tcttgcgcaa
2161 ggag (SEQ ID NO: 25)

MALSLLSVFII^hHFVFTNVVFAAS

45 NEESNALVSLPTPTLPSPSPA
TKPPSPALKPPTPSYKPPTLP
TTPIKPPTTKPPVKPPTIPVT
FVKPPVSTPPIKLPPVQPPY
KPPTPTVKPPSVQPPYKPPT
50 PTVKPPTTSFVKPPTTPPVQS
PPVQPPYKPPTSPVKPPTT
PPVKPPTTTPPVQPPTYNPPT
TPVKPPTAPFVKPPTPPFVRT
RID

55

CVPLCGTRCGQHSRKNVCMRACVTCCYRCKCVPPGTYGNKEKCGSCYANMKTRGGKSKCP* (SEQ ID NO: 26)

M. At5g59845

5 1 gacttgagta tgaatccaat aacccaaaat ttatgcagat tttagaatac ttcttataaa
61 tctttaaata ataacacaaa actttaacat actttaaca aatcttgatt gaataacaac
121 agattctaca tgacatttta aatcactaaa actcttttga aatcataaac caataacaac
181 cccttagttt ttactatatt gaattctgac gtactttttt attagttgaa ttctataaaa
241 tgagaaaaca ttaattatct cttaatcttt gaacttaagc cccacaaaaa tcttataaat
10 301 tgggacagat ggactagata acaagcgttt cacctactcc aaaatttccc tataagtaac
361 tcttttttga acctcctttt cttcccaaac catcactcct ttgcatgtgt gtgaaacctt
421 cgagttttct cttcatcttc tcaaagtaac aaactttctc caaacagatt attattaaaa
481 caatctcatc aagaactacg ATGAAATTCC CGGCTGTAAA AGTTCTTATT ATCTCTCTC
541 TCATCACATC TTCTTTGTTC ATACTCTCAA CCGCGGATTC GTgtaagtat acacaatgca
15 601 ttttcttatt ttagatactt ttctcattag aaatttagct ttcttaataa aattgtattg
661 tgatgatgga ttaattagCA CCATGCGGAG GAAATGCAA CGTGAGATGT TCAAAGGCAG
721 GAAGACAAGA TAGGTGTCTC AAGTATTGTA ATATATGTTG CGAGAAGTGT AACTATTGTG
781 TTCCTTCAGG CACTTATGGA AACAAAGATG AATGCCCTTG TTACCGCGAT ATGAAGAACT
841 CCAAAGGCAC GTCCAAATGT CCTTGATcat gttcttaaga ttatccttat agacacaata
20 901 tcttgaaatg ttaagattgt gcttgatgcc taaaataatg agcttgagat acttctatga
961 atgaatatgt gaaagatttt gacaataaaa tgatttgatg tattaaaaa ttcttagtga
1021 agttatatat gtataaatga agtatgaaat atacattgta tgttgcttta catgagaaag
1081 ataaatctac aacaatccaa tgtatgaaaa ttttactaag ttaactgac agaaacgtta
1141 attatgggtt agaactctgt ggagagatga ttacttttgt aagagaaatt gattgtttgt
1201 tgtcaatgag gataaagtaa gaagccattt ctcaacacat ggacttgata gcaaaactaaa
25 1261 caaggctcaa gcattgaaat tgaaaacgtc cgatagataa gattggctca agaaaagcaa
1321 gtgttttttg ttgtagaaaa cagaaattga aattactgtc tacttt (SEQ ID NO: 27)

30 MKFPAVKVLIISLLITSSLFILSTA

DSSP

35 CGGKCNVRCSKAGRQDRCLKYCNICCEKCNVCVPSGTYGNKDECPCYRDMKNSKGTSKCP* (SEQ ID NO: 28)

N. At3g10170

genomic structure before splicing and processing 5'- towards 3'
predicted orf sequences are underlined

5

CTGTTTCAGAAAATGGCAACAAACTTAGCATCATTGTTTCTCCATTG
TTGTGTTACATCTTCTTCTGTCTGCCCATATGCATGTAAGTGTTTCAACA
CTCTATTCCCTCTATGTTTCACATTTATCAACTTTATCTTATACGTCCTGA
ATAAAACACAGCCTATATACCTGGAACTCTCTGCTCGACAACCACAACCA
10 CCACAGTCGCAACCACAACCTGCCGCATCACAATAACTCTCAAGTGAGTTT
CTCGGTTTCATCACTACTCAAAAAAAGAGTTTCATCGAATCTACAAAACCT
TTTTAACATCCTTTGCATCTTCTGTGATTTTGGCAGTACGGTACTACT
CAAGGCAGTCTTCAACCCCAAGGTAAACCCACTGACTAGCCTAGTTTTTA
15 ATTAATGTTTGTGCTGAATGCGAACTAATCCGCTATTCCACCTTTATT
AGAGTGCGGGCCAAGGTGTGSAGATAGATGCTCGAATACACAATACAAGA
AGCCGTGTTTGTCTTCTGCAACAATGTTGTAACAAGTGCTTGTGTGTG
CCCCAGGTACTTATGGCAATAAGCAAGTATGCTTGTCTATAACAACCTG
GAAGACCAAGAGCGGTGGACCAAAATGCCCTTAGTTTCTCCTCTTAATTA
20 CTTTAGCATAAACTCCATGTAATTTGTTAATCTACCTATCATAATTATA
TATGATTGGACTCTTCCATAATCACATCAGTTCTCTGTGATTATGACGT (SEQ ID NO: 29)

Amino acid sequence of the predicted pre-pro-peptide
the first line represents the signal sequence
the second (set of) lines represents the the pro-peptide
25 the last line represents the conserved Cysteine motif.

MATKLSIIVFSIVVLHLLLSAHMH

30 FLINVCAECETKSAIPPLLE

CGPRCGDRCSNTQYKKPCLFFCNKCCNKCLCVPPGTYGNKQVCPYNNWTKSGGPKCP* (SEQ ID NO: 30)

35

They consist of an N-terminal signal peptide, followed by a variable domain (involved in mobility or cell wall attachment) and a C-terminal domain with 12 conserved cystein residues. The consensus of this last domain is:

C-C-RC-----C---C--CC-(R/K)C-CVP(P/S)GT-G(N/H)---C-CY-----G--KCP* (SEQ ID NO: 31)

(-) = any amino acid;
 (C) = conserved C-residue
 (/) = either one or the other amino acid at this position;
 * = stopcodon

Some members of this gene family have been described previously, and represent the GASA family in *Arabidopsis thaliana* (Plant Mol. Biol. 36 (1998). Similar family members containing the same structural motifs are present in rice (like GASR1) and tomato (Plant Journal 2 (1992) 153-159; Mol. Gen. Genet. 243 (1994) Taylor and Scheuring). In *Arabidopsis*, the GASA gene family represents 14 different members, similar as the number for the RKS gene family. Our data on the similar phenotypes for RKS4 and GASA3 (figure 6) and the fact that there are similar numbers of ligands and receptors suggest that there is a single GASA ligand molecule interaction with a single RKS molecule. T-DNA knock out phenotypes observed with several of the other GASA peptide ligand genes also show modifications of organ and plant size like the appearance of extreme dwarf plants resembling brassinosteroid insensitive mutants. Co-localization of RKS genes and GASA ligands on the genome (see figure 4) could provide clues of molecular interactions between GASA molecules and RKS molecules (similar as for S locus proteins and S locus receptor kinases).

Furthermore, in the chapter discussing the effects of roots in RKS transgenic plants, it was shown that overexpression of RKS genes can result in the formation of lateral roots (figure 26). One of the GASA ligands is involved in the formation and/or outgrowth of lateral roots as discussed in Mol. Gen. Genet. 243, 1994, 148-157.

Intracellularly, this signal is transmitted onto membrane (but not necessarily plasma membrane) associated NDR-NHL proteins. At least some of the functions of the syntaxin-like NDR-NHL

5 proteins would thereby result in the regulation of vesicle transport and /or the positioning of new cell wall formation. Neighboring cells are known to influence and determine the developmental state and the differentiation of cells. In transgenic plants with RKS and / or NDR-NHL expression

10 cassettes the positioning of new cell walls is modified, resulting in abnormal neighboring cells, resulting in abnormal development of groups of cells like flower meristem primordia as observed and shown with RKS0, RKS13 and NHL10.

Table 2 overview of accessions numbers of RKS signal complex genes in arabidopsis and in rice:

Gene code	contig	gene prediction in At database	Oryza sativa japonica contig	approximate position in bp around:
RKS0 At1g71830	f14c23	ok	OSJNBa0036B21	52.000
RKS1 At1g60800	f8a5	ok	P0038C05	60.000
RKS2 At5g65240	mgn23	ok	OJ1212_C08	8000
RKS3 At5g63710	mbk5	ok	see rks2	
RKS4 At2g23950	t29e15	wrong, exon missing	P0708B04	35.000
RKS5 At5g45780	mra19	wrong, exon missing	OJ1077_A12	102.000
RKS6 At5g10290	wt e 23	ok	see rks2	
RKS7 At5g16000	ku e 24	ok	P0038C05	60.000
RKS8 At1g34210	f23ml9	ok	OJ1134_B10	90.000 & 1000 2
different genes!				
RKS10 At4g33430	en d 25	wrong, exon missing	see rks0	
RKS11 At4g30520	wu d 20	wrong, exon missing	see rks4	
RKS12 At2g13800	f13j11	wrong, exon missing	see rks10	
RKS13 At2g13790	f13j11	ok	P0633E08	36.000
RKS14 At3g25560	mw12	wrong, exon missing	OSJNBb0015G09	36.000
ELS1 At5g21090	ch e 52	ok	P0003H10	53.000
ELS2 possibly allelic variant of ELS1 no genomic sequence identified yet				see els1
ELS3 At3g43740	by c 21	ok	P0468B07	52.000

Homology between aa sequences from arabidopsis proteins are compared with the rice databases using:
http://mips.gsf.de/proj/thal/db/search/search_frame.html
 protein sequences based on Oryza sativa japonica contig sequences.

Arabidopsis thaliana ELS1 cDNA

The start codon encoding the first predicted methionine
5 residue of the gene product has been indicated by bold
capitals.

The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in
capitals. Leader and trailer sequences are in lowercase
10 letters.

```
ttactctcaaattccttttcgatttcctctcttaaacctccgaaagctcac
ATGGGCTCTCGAACTATCGGTGGGAGCTCTTCGCAGCTTCGTTAACCCCTAA
CCTTAGCTTTGATTACCTGGTCGAAGCAAACCTCCGAAGGAGATGCTCTCTA
15 CGCTCTTCGCCGGAGTTTGACAGATCCAGACCATGTCTCCAGAGCTGGGAT
CCAACTCTTGTTAATCCTTGTAACCTGGTTCCATGTCACCTGTAACCAAGACA
ACCGCGTCACTCGTGTGGATTGGGAAATTCAAACCTCTCTGGACATCTTGC
GCCTGAGCTTGGAAGCTTGAACATTACAGTATCTAGAGCTCTACAAAAC
AACATCCAAGGAATAACCTTCGAACTTGGAATCTGAAGAATCTCATCA
20 GCTTGGATCTGTACAACAACATCTTACAGGGATAGTCCCACTTCTTTGGG
AAAATGAAGTCTCTGGTCTTTTACGGCTTAATGACAACCGATTGACGGTC
CAATCCCTAGAGCACTCACGGCAATCCCAAGCCTTTAAAGTTGTGACGTCTC
AAGCAATGATTTGTGTGGACAATCCACAAACGGACCCTTTGCTCACATTCC
TTTACAGAACTTTGAGAACAACCCGAGATTGGAGGGACCGGAATTACTCGGT
25 CTTGCAAGCTACGACACTAACTGCACCTGAaacaactggcaaacctgaaat
gaagaattgggggtgaccttgaagaacacttcaccactttatcaaatatc
acatctactatgtaataagtatatatatgtagtccaaaaaaaaaaaaaaaaa (SEQ ID NO: 32)
```

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS1
30 protein.

Different domains are spaced and shown from the N-terminus
towards the C-terminus. Overall domain structure is similar as
described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain
35 represents a signal sequence. The second domain contains a
leucine zipper motif, containing 4 leucine residues, each
separated by seven other amino acids. The third domain
contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich

repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

5

MASRNYRWELFAASL
TLTLALIHLEVEANSEG

DALYALRRSLTDP

10 DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

DLGNSNLSGHLA

15 P ELGKLEHLQYLELYKNNIQGTI

PSELGNLKNLISLDLYNNNLTGIV

PTSLGKLKSLVFLRLNDNRLTGPI

PRALTAIPSLKVVDVSSNDLCGTI

PTNGPFAHIPLQNFENNPRLEGPE

20

LLGLASYDTNCT (SEQ ID NO: 33)

Arabidopsis thaliana ELS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 aaaattactcaaattcctattagattactctcttcgacctccgatagctcac
ATGGCGTCTCGAACTATCGGTGGGAGCTCTTCGCAGCTTCGTTAATCCTAA
CCTTAGCTTTGATTACCTGGTGAAGCAAACCTCCGAAGGAGATGCTCTTTA
CGCTCTTCGCCGGAGTTTAAACAGATCCGGACCATGTCCTCCAGAGCTGGGAT
CCAACCTCTGTTAATCCTTGTACCTGGTCCATGTACCTGTAACCAAGACA
15 ACCGCGTCACTCGTGTGGATTGGGGAATCAAACCTCTCTGGACATCTTGC
GCCTGAGCTTGGGAAGCTTGAACATTTACAGTATCTAGAGCTCTACAAAAC
AACATCCAAGGAACATAACCTCCGAACCTGGAAATCTGAAGAATCTCATCA
GCTTGGATCTGTACAACAACATCTTACAGGGATAGTTCCCACTTCTTTGGG
AAAATTGAAGTCTCTGGTCTTTTACGGCTTAATGACAACCGATTGACGGGG
20 CAATCCCTAGAGCACTCACTGCCAATCCCAAGCCTTAAAAGTTGTGGATGTC
TAAGCAATGATTTGTGTGGAACAATCCCAACAACGGACCTTTTGCTCACAT
TCCTTTACAGAACCTTTGAGAACAACCCGAGGTTGGAGGGACCGGAATTACTC
GGTCTTGCAAGCTACGACACTAACTGCACCTGAagaaattggcaaaacctga
aaatgaagaattgggggggaccttgtaagaacacttcaccactttatcaaat
25 atcacatctactatgtaataagtatatatatgtagtccaaaaaaaaaatgaa
gaatcgaatagtaatatcatctggtctcaattgagaactttgaggtctgtgt
atgaaaattaaagattgtactgtaatgttcggttggtggtgattctgagaagta
acatttgattggtatggtatcaagttgttctgccttgctctgcaaaaaaaaa (SEQ ID NO: 34)

30

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS2 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as
35 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino acids. The third domain

contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The last domain might be
5 involved in attachment to other proteins or structures within the cell wall.

MASRNYRWELFAASL
ILTLALIHLEVEANSEG

10

DALYALRRSLTDP
DHVLQSWDPTLVN

PCTWFHVTCNQDNRVTRV

15

DLGNSNLSGHLA

P ELGKLEHLQYLQLYKNNIQGTI
PSELGNLKNLISLDLYNNNLTGIV
PTSLGKLKSLVFLRLNDNRLTGPI
20 PRALTAIPSLKVVDVSSNDLCGTI
PTNGPFAHIPLQNFENNPRLEGPE

LLGLASYDTNCT (SEQ ID NO: 35)

25

Arabidopsis thaliana ELS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ttctctctccggcgaaaacc**ATGGTGGCGCAAACAGTCGGCGGGAGCTTCTAGCAGCTT**
 CCCTGATCCTAACTTTAGCTCTAATTCGTCTAACGGAAGCAAAC**TCCGAAGGGGACGCTC**
 TTCACGCGCTTCGCCGGAGCTTATCAGATCCAGACAATGTTGTT**CAGAGTTGGGATCCAA**
 CTCTTGTTAATCCTTGTA**CTTGGTTTCATGTCACTTGTAATCAACACCATCAAGTCACTC**
 GTCTGGATT**TGGGAATTCAA**CTTATCTGGACATCTAGTACCTGA**ACTTGGGAAGCTTG**
 15 AACATTTACAATATCTTGA**ACTCTACAAAACGAGATTCAAGGA**CTATACCTTCTGAGC
 TTGGAAATCTGAAGAGTCTAATCAGTTTGGATCTGTACAACA**CAATCTCACCGGGAAAA**
 TCCCATCTTCTTTGGGAAAT**TGAAGCGGCTTAACGAAAACCGATTGACCGGTCCTATTC**
 CTAGAGAACTCACAGTTATTTCAAGCCTTAAAGTTGTTGATGTCTCAGGGAATGATTTGT
 GTGGAA**CAATTC**CAGTAGAAGGACCTTTTGAACACATTCC**TATGCAAACTTTGAGAACA**
 20 ACCTGAGATTGGAGGGACCA**GA**CTACTAGGTCTTGC**GAGCTATGACACCAATTGCACTT**
AAaaagaagttgaagaa (SEQ ID NO: 36)

Predicted amino acid sequence of the *Arabidopsis thaliana* ELS3 protein.

25 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt *et al.* (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a

30 leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each
 35 approximately 24 amino acid residues. The last domain might be involved in attachment to other proteins or structures within the cell wall.

MVAQNSRRELLAASL
ILTIALIRLTEANSEG

5 DALHALRRSLSDP
DNVVQSWDPTLVN

PCTWFHVTCNQHHQVTRL

DLGNSNLSGHLV
10 P ELGKLEHLQYLELYKNEIQGTI
PSELGNLKSLSLDLYNNNLTKI
P SSLGKLKRLNENRLTGPI
PRELTVISSLKVVDVSGNDLCGTI
PVEGPFHEIPMQNFENNLRLLEGPE
15 LLGLASYDTNCT (SEQ ID NO: 37)

Arabidopsis thaliana RKS0 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 atttttatttttattttttactctttgtttgttttaatgctaattgggtttttaaaagggtt
atcgaaaaaatgagtgagtttggttgaggttgctctgttaaagtgttaatggtggtgat
tttcggaagttagggttttctcggatctgaagagatcaaatcaagattcgaaatttacca
ttgttggttgaa**ATGGAGTCGAGTTATGTGGTGT**TTATCTTACTTTCCTGATCTTACTT
CCGAATCATTCACTGTGGCTTGCTTCTGCTAATTTGGAAGGTGATGCTTTCATACTTTG
15 AGGGTTACTCTAGTTGATCCAAACAATGTCTTGCAAGAGCTGGGATCCTACGCTAGTGAAT
CCTTGACATGGTTCCATGTCATTGCAACAACGAGAACAGTGTCTAAGAGTTGATTTG
GGGAATGCAGAGTTATCTGGCCATTTAGTTCCAGAGCTTGGTGTGCTCAAGAATTTGCAG
TATTTGGAGCTTTACAGTAACAACATAACTGGCCCGATTCTAGTAATCTTGGAAATCTG
ACAAACTTAGTGAGTTTGGATCTTTACTTAAACAGCTTCTCCGGTCTATTCCGGAATCA
20 TTGGGAAAGCTTTCAAAGCTGAGATTTCTCCGGCTTAACAACAACAGTCTCACTGGGTCA
ATTCTATGTCACTGACCAATATTACTACCCTTCAAGTGTAGATCTATCAAATAACAGA
CTCTCTGGTTCAGTTCCTGACAATGGCTCCTTCTCACTCTTCACACCCATCAGTTTGTCT
AATAACTTAGACCTATGTGGACCTGTTACAAGTCACCCATGTCTGGATCTCCCCGTTT
TCTCTCCACCACCTTTTATTCAACCTCCCCAGTTTCCACCCCGAGTGGGTATGGTATA
25 ACTGGAGCAATAGCTGGTGGAGTTGCTGCAGGTGCTGCTTTGCCCTTTGCTGCTCCTGCA
ATAGCCTTTGCTTGGTGGCGACGAAGAAGCCCACTAGATATTTCTTCGATGTCCCTGCC
GAAGAAGATCCAGAAGTTCATCTGGGACAGCTCAAGAGGTTTCTTTGCGGGAGCTACAA
GTGGCGAGTGATGGGTTTAGTAACAAGAACATTTTGGGCAGAGGTGGGTTTGGGAAAGTC
TACAAGGGACGCTTGGCAGACGGAACCTTGTGTGCTGTCAAGAGACTGAAGGAAGAGCGA
30 ACTCCAGGTGGAGAGCTCCAGTTTCAAACAGAAGTAGAGATGATAAGTATGGCAGTTCAT
CGAAACCTGTTGAGATTACGAGGTTTCTGTATGACACCGACCGAGAGATTGCTTGTGTAT
CCTTACATGGCCAATGGAAGTGTGCTTCGTGTCTCAGAGAGAGGCCACCGTCACAACCT
CCGCTTGATTGGCCAACGCGGAAGAGAATCGCGCTAGGCTCAGCTCGAGGTTTGTCTTAC
CTACATGATCACTGCGATCCGAAGATCATTCACCGTGACGTAAAAGCAGCAAACATCCTC
35 TTAGACGAAGAATTCTGAAGCGGTTGTTGGAGATTTCCGGTTGGCAAAGCTTATGGACTAT
AAAGACACTCACGTGACAACAGCAGTCCGTGGCACCATCGGTACATCGCTCCAGAATAT
CTCTCAACCGGAAAATCTTCAGAGAAAACCGACGTTTTCCGATACGGAATCATGCTTCTA
GAACTAATCACAGGACAAAGAGCTTTCGATCTCGCTCGGCTAGCTAACGACGACGAGTC
ATGTTACTTGAAGGATTGTTGAAGGAGAAGAAGCTAGAGATGTTAGTGGAT
40 CCAGATCTTCAAACAACTACGAGGAGAGAGAACTGGAACAAGTGATACAAGTGGCGTTG

CTATGCACGCAAGGATCACCAATGGAAAGACCAAAGATGTCTGAAGTTGTAAGGATGCTG
GAAGGAGATGGGCTTGCGGAGAAATGGGACGAATGGCAAAAAGTTGAGATTTTGAGGGAA
GAGATTGATTTGAGTCCTAATCCTAACTCTGATTGGATTCTTGATTCTACTTACAATTTG
CACGCCGTTGAGTTATCTGGTCCAAGGTAAaaaaaaaaaaaaaaaaaaaaa (SEQ ID NO: 38)

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS0 protein.

Different domains are spaced and shown from the N-terminus
10 towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino
15 acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline
20 residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also
25 containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MESSYVVFILLSLILLPNHSL
WLASANLEG

DALHTLRVTLVDP

35

NNVLQSWDPTLVN

PCTWEHVTCNNENSVIRV

DLGNAELSGHLV

40

P ELGVLKNLQYLELYSNNITGPI

PSNLGNLTNLVSLDLYLNSFSGPI
PESLGKLSKLRFLRLNNSLTGSI
PMSLTNITTQVLDLSNNRLSGSV
PDNGSFSLETPISFANNLDLCGPV
5
TSHPCPGSPFFSPPPP
FIQPPPVSPTSOGYGITG

AIAGGVAAGAAL
10 PFAAPAIAFAWW

RRRKPLDIFFDVPAAEDPE
VHLGQLKRFSLRELQVAS

15 DGFSNKNILGRGGFGKVYKGRAD
GTLVAVKRLKEERTPGGELQFQ
TEVEMISMAVHRNLLRLRGFCM
TPTERLLVYPYMANGSVASCLR
ERPPSQPPLDWPTRKRIALGSA
20 RGLSYLHDHCDPKIIHRDVKAA
NILLDEEFEAVVGDFGLAKLMD
YKDTHTTAVRGTTIGHIAPEYL
STGKSSEKTDVFGYGIMLELI
TGQRAFDLARLANDDDVMLLDW
25 VKGLLKEKKLEMLVDPDLQTN
EERELEQVIQVALLCTQGSPME
RPFMSEVVRMLE

GDGLAEKWDEWQKVEILREEIDLS
30
PNPNSDWILDSTYNLHVELSGPR (SEQ ID NO: 39)

Arabidopsis thaliana RKS1 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ccaaagttgattgctttaagaagggat**ATGGAAGGTGTGAGATTTGTGGTGTGGAGATTA**
GGATTTCTGGTTTTTGTATGGTTCTTTGATATCTTCTGCTACACTTTCTCCTACTGGT
GTAAACTATGAAGTGACAGCTTTGGTTGCTGTGAAGAATGAATTGAATGATCCGTACAAA
GTTCTTGAGAATTGGGATGTGAATCAGTTGATCCTTGTAGCTGGAGAATGGTTTCTTGC
ACTGATGGCTATGTCTCTTCACTGGATCTTCCTAGCCAAAGCTTGCTGGTACATTGTCT
15 CCTAGAATCGGAAACCTCACCTATTTACAATCAGTGGTGTGCAAAACAATGCAATCACT
GGTCCAATTCGGGAAACGATTGGGAGGTGGAGAAGCTTCAGTCACTTGATCTTTCGAAC
AATTCATTACCGGGGAGATACCGGCCTCACTTGAGAACTCAAGAACTTGAATTACTTG
CGGTTAAACAATAACAGTCTTATAGGAAGTTGCCCTGAGTCTCTATCCAAGATTGAGGGA
CTCACTCTAGTCGACATTTTCGTATAACAATCTTAGTGGTTCGCTGCCAAAAGTTTCTGCC
20 AGAACTTTCAAGGTAATTGGTAATGCGTTAATCTGTGGCCCAAAGCTGTTTCAAAGTGT
TCTGCTGTTCCCGAGCCTCTCACGCTCCACAAGATGGTCCAGATGAATCAGGAACTCGT
ACCAATGGCCATCACGTTGCTCTTGCATTTGCCGCAAGCTTCAGTGCAGCATTTTTTGGT
TTCTTTACAAGCGGAATGTTTCTTTGGTGGAGATATCGCCGTAACAAGCAAATATTTTTT
GACGTTAATGAACAATATGATCCAGAAGTGAGTTTAGGGCACTTGAAGAGGTATACATTC
25 AAAGAGCTTAGATCTGCCACCAATCATTTCAACTCGAAGAACATTCTCGGAAGAGGCGGA
TACGGGATTGTGTACAAAGGACACTTAAACGATGGAACCTTTGGTGGCTGTCAAACGTCTC
AAGGACTGTAACATTGCGGGTGGAGAAGTCCAGTTTCAGACAGAAGTAGAGACTATAAGT
TTGGCTCTTCATCGCAATCTCCTCCGGCTCCGCGGTTTCTGTAGTAGCAACCAGGAGAGA
ATTTTAGTCTACCCTTACATGCCAAATGGGAGTGTGCATCACGCTTAAAGATAATATC
30 CGTGGAGAGCCAGCATTAGACTGGTCGAGAAGGAAGAAGATAGCGGTTGGGACAGCGAGA
GGACTAGTTTACCTACAGGAGCAATGTGACCCGAAGATTATACACCGCGATGTGAAAGCA
GCTAACATTCTGTAGATGAGGACTTCGAAGCAGTTGTTGGTGATTTTGGGTTAGCTAAG
CTTCTAGACCATAGAGACTCTCATGTCACAACTGCAGTCCGTGGAAGTGTGGCCACATT
GCACCTGAGTACTTATCCACGGGTGAGTCTCAGAGAAGACTGATGTCTTTGGCTTTGGC
35 ATACTTCTCCTTGAGCTCATTACTGGTCAGAAAGCTCTTGATTTTGGCAGATCCGCACAC
CAGAAAGGTGTAATGCTTGACTGGGTGAAGAAGCTGCACCAAGAAGGGAACTAAAGCAG
TTAATAGACAAAGATCTAAATGACAAGTTCGATAGAGTAGAACTCGAAGAAATCGTTCAA
GTTGCGCTACTCTGCACTCAATTCAATCCATCTCATCGACCGAAAATGTCAGAAGTTATG
AAGATGCTTGAAGGTGACGGTTTGGCTGAGAGATGGGAAGCGACGCAGAACGGTACTGGT
40 GAGCATCAGCCACCGCCATTGCCACCGGGATGGTGAGTTCTTCGCCGCGTGTGAGGTAT

TACTCGGATTATATTCAGGAATCGTCTCTTGTAGTAGAAGCCATTGAGCTCTCGGGTCCT
CGATGAttatgactcactgtttttaaaaa (SEQ ID NO: 40)

- 5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS1 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

- 10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-
20 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MEGVREFVVWRLGFL
VFVWFFDISSATLSPTGVNIEV

TALVAVKNELNDP

35

YKVLNWDVNSVD

PCSWRMVSCDGYVSSL

DLPSQSLSGT
LSPRIGNLTYLQSVLQNNAITGPI
PETIGRLEKLQSLDLSNNSFTGEI
PASLGELKNLNYLRRLNNSLIGTC
5 PESLSKIEGLTLVDISYNNLSGSL
PKVSARTFK VIGNALICGPK

AVSNCSAVPEPLTL
PQDGPDESGTRTNG
10
HHVALAFAASFS
AAFFVFFFTSGMFLWW

RYRRNKQIFFDVNEQYDPE
15 VSLGHLKRYTFKELRSAT

NHFNSKNILGRGGYGIVYKGHLND
GTLVAVKRLKDCNIAGGEVQFQ
TEVETISLALHRNLLRLRGFCS
20 SNQERILVYPMPNGSVASRLK
DNIRGEPALDWSRRKKIavgTA
RGLVYLHEQCdPKIHRDVkaa
NILDEDFEAVVGDFGLAKLLD
HRDSHVTTAVRGTVGHIAPEYL
25 STGQSSEKTDVFGFGILLLELI
TGQKALDFGRSAHQKGVMLDW
VKKLHQEGKLKQLIDKDLNDKF
DRVELEEIVQALLCTQFNPSH
RPKMSEVMKMLE
30
GDGLAERWEATQNGTGEHQPPPLPPGMVSSS

PRVRYYSdYIQESSLVVEAIELSGPR (SEQ ID NO: 41)
35

Arabidopsis thaliana RKS2 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

Italics indicate the presence of an alternatively spliced gene product.

10

tcaat^{ttt}ggtagctccttagaaaa**ATGG**CTCTGCTTATTATCACTGCCTTAGT^{TTTT}TAGT
AGTTTATGGTCATCTGTGTACCAGATGCTCAAGGGGATGCATTATTGCGTTGAGGAGC
TCGTTACGTGCATCTCCTGAACAGCTTAGTGATTGGAACCAGAATCAAGTCGATCCTTGT
ACTTGGTCTCAAGTTATTTGTGATGACAAGAAACATGTTACTTCTGTAACCTTGTCTTAC

15

ATGAAC^{TTCT}CCTCGGGAACACTGTCTTCAGGAATAGGAATCTTGACAAC^{CTCT}CAAGACT
CTTACATTGAAGGGAAATGGAATAATGGGTGGAATACCAGAATCCATTGGAAATCTGTCT
AGCTTGACCAGCTTAGATTGGAGGATAATCACTTAACTGATCGCATTCATCCACTCTC
GGTAATCTCAAGAATCTACAGTTCTTCAGGACCTTGAGTAGGAATAACCTTAATGGTTCT
ATCCCGGATTCACTTACAGGTCTATCAAACTGATAAATATTCTGCTCGACTCAAATAAT

20

CTCAGTGGTGTAGATTCTCAGAGTTTATTCAAAATCCCAAAATACAATTTACAGCAAAC
AACTTGAGCTGTGGTGGCACTTTCCCGCAACCTTGTTAACCAGTCCAGTCCTTCAGGT
GATTCAAGCAGTAGAAAACTGGAATCATCGCTGGAGTTGTTAGCGGAATAGCGGTTATT
CTACTAGGATTCTTCTTCTTTTCTTCTGCAAGGATAAACATAAAGGATATAAACGAGAC
GTATTTGTGGATGTTGCAGGAACGAAC^{TTTAAAAA}AGGTTGATTTCAAGGTGAAGTGGAC

25

AGAAGGATTGCTTTTGGACAGTTGAGAAGATTGCATGGAGAGAGCTTCAGTTGGCTACA
GATGAGTTCAAGTGAAGAAGATGTTCTCGGACAAGGAGGCTTTGGGAAAGTTTACAAAGGA
TTGCTTTTCGGATGGCACC^{AAAGT}CGCTGTAAAAAGATTGACTGATTTGAACGTCCAGGA
GGAGATGAAGCTTTCCAGAGAGAAGTTGAGATGATAAGTGTAGCTGTTCATAGGAATCTG
CTTCGCCTTATCGGCTTTTGTACACACAACTGAACGACTTTTGGTGTATCCTTTCATG

30

CAGAATCTAAGTGTTCATATTGCTTAAGAGAGATTAAACCCGGGGATCCAGTTCTGGAT
TGGTTCAAGGAGAAACAGATTGCGTTAGGTGCAGCACGAGGACTCGAATATCTTCATGAA
CATTGCAACCCGAAGATCATACACAGAGATGTGAAAGCTGCAAATGTGTTACTAGATGAA
GACTTTGAAGCAGTGGTTGGTGATTTTGGTTTAGCCAAGTTGGTAGATGTTAGAAGGACT
AATGTAACCACTCAGGTCCGAGGAACAATGGGTCATATTGCACCAGAATGTATATCCACA

35

GGGAAATCGTCAGAGAAACCGATGTTTTCGGGTACGGAATTATGCTTCTGGAGCTTGT
ACTGGACAAAGAGCAATTGATTTCTCGCGGTTAGAGGAAGAAGATGATGTCTTATTGCTA
GACCATGTGAAGAACTGGAAAGAGAGAAGAGATTAGAAGACATAGTAGATAAGAAGCTT
GATGAGGATTATATAAAGGAAGAAGTTGAAATGATGATACAAGTAGCTCTGCTATGCACA
CAAGCAGCACCGGAAGAACCAGACGCGATGTCGGAAGTAGTAAGAATGCTAGAAGGAGAA

40

GGGCTTGCAGAGAGATGGGAAGAGTGGCAGAATCTTGAAGTGACGAGACAAGAAGAGTTT

CAGAGGTTGCAGAGGAGATTGATTGGGGTGAAGATTCCATTAATAATCAAGATGCTATT
GAATTATCTGCTGGAAGATAGaaacaaaaaa (SEQ ID NO: 42)

- 5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS2 protein.
- Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).
- 10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
- 15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 3 complete and 2 incomplete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site
- 20 for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
- 25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions. Italics indicate an alternatively spliced gene
- 30 product.

MALLIITALVFSSL

WSSVSPDAQG

35 DALFALRSSLR

ASPEQLSDWNQNQVD

PCTWSQVICDDKKHVTSV

T L S Y M N F S S G T L S S G I
G I L T T L K T L T L K G N G I M G G I
P E S I G N L S S L T S L D L E D N H L T D R I
5 P S T L G N L K N L Q F L T L S R N N L N G S I
 P D S L T G L S K L I N I L L D S N N L S G E I
 P Q S L F K I P K Y N F T A N N L S C G G

T F P Q P C V T E S S P S G D S S S R K T G
10
 I I A G V V S G I A V I L
 L G F F F F F F C

K D K H K G Y K R D V F V D V A G T N F K K G L I S G E
15 V D R R I A F G Q L R R F A W R E L Q L A T

D E F S E K N V L G Q G G F G K V Y K G L L S D
G T K V A V K R L T D F E R P G G D E A F Q
R E V E M I S V A V H R N L L R L I G F C T
20 T Q T E R L L V Y P F M Q N L S V A Y C L R
 E I K P G D P V L D W F R R K Q I A L G A A
 R G L E Y L H E H C N P K I I H R D V K A A
 N V L L D E D F E A V V G D F G L A K L V D
 V R R T N V T T Q V R G T M G H I A P E C I
25 S T G K S S E K T D V F G Y G I M L L E L V
 T G Q R A I D F S R L E E D D V L L L D H
 V K K L E R E K R L E D I V D K K L D E D Y
 I K E E V E M M I Q V A L L C T Q A A P E E
 R P A M S E V V R M L E
30
 G E G L A E R W E E W Q N L E V T R Q E E F Q

R L Q R R F D W G E D S I N N Q D A I E L S G G R (SEQ ID NO: 43)
35

Arabidopsis thaliana RKS3 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

aacggtgaaagtttccatgatcctcttcgaggattcattcaaagaaattgcttttagatgg
10 aacaatcagaaattgatcttacaatgtttc**ATGGCCTTAGCTTTGTGGGAATCACTTCG**
TCAACAAC**TCAACCAGATATCGAAGGAGGAGCTCTGTTGCAGCTCAGAGATTCGCTTAAT**
GATTCGAGCAATCGTCTAA**ATGGACACGCGATTTTGTGAGCCCTTGCTATAGTTGGTCT**
TATGTTACCTGCAGAGGCCAGAGTGT**TGTGGCTCTAAATCTTGCCTCGAGTGGATTCA**
GGAACACTCTCTCCAGCTATTACAA**ACTGAAGTTCTTGGTTACCTTAGAGTTACAGAAC**
15 AATAGTTTATCTGGTGCCTTACCAGATTCTCTTGGGAACATGGTTAATCTACAGACTTTA
AACCTATCAGTGAATAGTTT**CAGCGGATCGATACCAGCGAGCTGGAGTCAGCTCTCGAAT**
CTAAAGCACTTGGATCTCTCATCCAATAATTTAACAGGAAGCATCCCAACACAATTCTTC
TCAATCCCAACATTCGATTTT**TTCAGGAACCTCAGCTTATATGCGGTAAAAGTTTGAATCAG**
CCTTGTTCTTCAAGTTCTCGTCTTCCAGTCACATCCTCCAAGAAAAGCTGAGAGACATT
20 ACTTTGACTGCAAGTTGTGTTGCTTCTATAATCTTATTCCTTGGAGCAATGGTTATGTAT
CATCACCATCGCGTCCGCAGAACCAATACGACATCTTTTTT**GATGTAGCTGGGGAAGAT**
GACAGGAAGATTTCTTTGGACA**ACTAAAACGATTCTCTTTACGTGAAATCCAGCTCGCA**
ACAGATAGTTTCAACGAGAGCAATTTGATAGGACAAGGAGGATTTGGTAAAGTATACAGA
GGTTTGCTTCCAGACAAAACAAAAGTTGCAGTGAAACGCCTTGC**GGATTACTTCAGTCCT**
25 GGAGGAGAAGCTGCTTTCCAAAGAGAGATT**CAGCTCATAAGCGTTGCGGTTCA**AAAAAT
CTCTTACGCCTTATTGGCTTCTGCACA**ACTTCCTCTGAGAGAATCCTTGTTATCCATAC**
ATGGAAAATCTTAGTGTTGCATATCGACTAAGAGATT**TGAAAGCGGGAGAGGAAGGATTA**
GACTGGCCAACAAGGAAGCGTGTAGCTTTTGGTTCAGCTCACGGTTTAGAGTATCTACAC
GAACATTGTAAACCGAAGATCATACACCGCGATCTCAAGGCTGCAAACATACTTTTAGAC
30 AACAAATTTGAGCCAGTTCTTGGAGATTTCGGTTTAGCTAAGCTTGTGGACACATCTCTG
ACTCATGTCACAACTCAAGTCCGAGGCACAATGGGTCACATTGCGCCAGAGTATCTCTGC
ACAGGAAAATCATCTGAAAAAACCGATGTTTTTGGTTACGGTATAACGCTTCTTGAGCTT
GTTACTGGTCAGCGCGCAATCGATTTTTT**CACGCTTGAAGAAGAGGAAAATATTCTCTTG**
CTTGATCATATAAAGAAGTTGCTTAGAGAACAGAGACTTAGAGACATTGTTGATAGCAAT
35 TTGACTACATATGACTCCAAAGAAGTTGAAACAATCGTTCAAGTGGCTCTTCTCTGCACA
CAAGGCTCACCAGAAGATAGACCAGCGATGTCTGAAGTGGTCAAAATGCTTCAAGGGACT
GGTGGTTTGGCTGAGAAATGGACTGAATGGGAACA**ACTGAAGAAGTTAGGAACAAAGAA**
GCATTGTTGCTTCCGACTTTACCGGCTACTTGGGATGAAGAAGAAACCACCGTTGATCAA
GAATCTATCCGATTATCGACAGCAAGATGAagaagaaacagagagagaaagatatctatg
40 aaaa (SEQ ID NO: 44)

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS3 protein.

- 5 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a
10 leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 4 complete repeats of each
15 approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular
20 domains are positioned. The seventh domain has an unknown function. The eight domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth
25 domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

MALAFVGITSSSTQPDIEG

30

GALLQLRDSLNDSSNRL

KWTRDFVS

PCYSWSYVTCRGQSVVAL

35

NLASSGFTGTLS

P AITKLKFLVTLELQNNLSLGGAL

PDSLGNMNVNLQTLNLSVNSFSGSI

PASWSQLSNLKHLDLSSNNLTGSI
PTQFFSIPTFEFSGTQLICGKS

5 LNQPCSSSRLPVTSSKKKLAD

ITLTASCVASIIL
FLGAMVMYHHH

10

RVRRTKYDIFFDVAGEDDR
KISFGQLKRFSLEIQLAT

DSFNESNLIGQGGFGKVYRGLLPD

15 KTKVAVKRLADYFSPGGEAAFO
REIQLISVAVHKNLLRLIGFCT
TSERILVYPYMENLSVAYRLR
DLKAGEEGLDWPTRKRVAFGSA
HGLEYLHEHCNPKIIHRDLKAA

20 NILDNNFEPVLGDFGLAKLVD
TSLTHVTTQVRGTMGHIAPEYL
CTGKSSEKTDVFGYGITLLELV
TGQRAIDFSRLEEEENILLD
HIKKLLREQRLROIVDSNLTTY

25 DSKEVETIVQVALLCTQGSPED
RPAMSEVVKMLQ

GTGGLAEKWTEWEQLEEVNKEALLL

30 PTLPATWDEEETVDQESIRLSTAR (SEQ ID NO: 45)

Arabidopsis thaliana RKS4 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

- 5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

- 10 tcttccttctccttctcgtaatctaataagcttttc**ATGGTGGT**GATGAAGATATTC
TCTGTTCTGTTACTACTATGTTTCTTCGTTACTTGTCTCTCTTCTGAACCCAGAAAC
CCTGAAGTGGAGGCGTTGATAAACATAAAGAACGAGTTACATGATCCACATGGTGTTC
AAAACTGGGATGAGTTTCTGTGATCCTGTAGCTGGACTATGATCTCTGTTCTTCA
GACAACCTCGTAATTGGCTTAGGAGCTCCAAGTCAGTCTCTTCAGGAACTTTATCTGGG
15 TCTATTGGAAATCTCACTAATCTTCGACAAGTGTCAATACAGAAACAATAACATCTCCGGT
AAAATCCACCGGAGATTTGTCTCTTCCCAAATTACAGACTCTGGATTTATCCAATAAC
CGGTTCTCCGGTGAAATCCCCGGTCTGTAAACCAGCTGAGTAATCTCCAATATCTGTG
AACAACAACCTCATTATCTGGGCCCTTTCCTGCTTCTGTCTCAAATCCCTCACCTCTCT
TTCTTAGACTTGTCTTATAACAATCTCAGAGGTCCTGTTCCCTAAATTTCTGCAAGGACA
20 TTCAATGTTGCTGGGAACCCTTGATTTGTAAAAACAGCCTACCGGAGATTTGTTTCAGGA
TCAATCAGTGCAAGCCCTCTTCTGTCTCTTTACGTTCTTCATCAGGACGTAGAACCAAC
ATATTAGCAGTTGCACTTGGTGTAGCCTTGGCTTTGCTGTTAGTGTAATCCTCTCTCTC
GGGTTCAATTGGTATCGAAAGAAACAAAGACGGTTAACGATGCTTCGCATTAACAAGCAA
GAGGAAGGGTTACTTGGGTTGGGAAATCTAAGAAGCTTCACATTAGGGAACCTCATGTA
25 GCTACGGATGGTTTtagttccaagagtattcttggTGCTGGTGGGTTTGGTAATGTCTAC
AGAGGAAAATTCGGGGATGGGACAGTGGTTGCAGTGAAACGATTGAAAGATGTGAATGGA
ACCTCCGGGAACCTCACAGTTTCGTACTGAGCTTGAGATGATCAGCTTAGCTGTTTCATAGG
AATTTGCTTCGGTTAATCGGTTATTGTGCGAGTTCTAGCGAAAGACTTCTTGTTTACCTT
TACATGTCCAATGGCAGCGTCGCCTCTAGGCTCAAAGCTAAGCCAGCGTTGGACTGGAAC
30 ACAAGGAAGAAGATAGCGATTGGAGCTGCAAGAGGGTTGTTTTATCTACACGAGCAATGC
GATCCCAAGATTATTCACCGAGATGTCAAGGCAGCAAACATTCTCCTAGATGAGTATTTT
GAAGCAGTTGTTGGGGATTTTGGACTAGCAAAGCTACTCAACCACGAGGATTCACATGTC
ACAACCGCGGTTAGAGGAACTGTTGGTCACATTGCACCTGAGTATCTCTCACCGGTCAG
TCATCTGAGAAAACCGATGTCTTTGGGTTCCGTATACTTTTGCTAGAGCTCATCACAGGA
35 ATGAGAGCTCTCGAGTTTGCCAAGTCTGTTAGCCAGAAAGGAGCTATGCTAGAATGGGTG
AGGAAGCTACACAAGGAAATGAAAGTAGAGGAGCTAGTAGACCGAGAACTGGGGACAACC
TACGATAGAATAGAAGTTGGAGAGATGCTACAAGTGGCACTGCTCTGCACTCAGTTTCTT
CCAGCTCACAGACCCAAAATGTCTGAAGTAGTTCAGATGCTTGAAGGAGATGGATTAGCT
GAGAGATGGGCTGCTTCACATGACCATTACATTTCTACCATGCCAACATGTCTTACAGG
40 ACTATTACCTCTACTGATGGCAACAACCAACCAACATCTGTTTGGCTCCTCAGGATTT

GAAGATGAAGATGATAATCAAGCGTTAGATTCATTCGCCATGGAAGTATCTGGTCCAAGG
TAGtaaatcttggacacagaaagaaacagatataatatcccatgacttcaatttttgtt (SEQ ID NO: 46)

5 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS4 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

10 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 2 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
15 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-
20 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
25 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30

MVVMKLITMKIFSVLLLL
CFFVTCSLSSEPRNPEV

EALINIKNELHDP

35

HGVFKNWDEFSD

PCSWTMISCSSDNLVIGL

GAPSQSLSGTLS

G SIGNLTNLRQVSLQNNNISGKI
PPEICSLPKLQTLDLNNRFSGEI
PGSVNQLSNLQYLRNLNNNSLSGPF
5 PASLSQIPHLSFLDLSYNNLRGPV
PKFPARTFNVAGNPLICKNS

LPEICSGSISASPL
SVSLRSSSGRRTN

10

ILAVALGVSLGFAVSVIL
SLGFIWY

RKKQRRLTMLRINKQEE
15 GLLGLGNLRSFTFRELHVAT

DGFSSKSILGAGGFGNVYRGKFGD
GTVVAVKRLKDVNGTSGNSQFR
TELEMISLAVHRNLLRLIGYCA
20 SSSERLLVYPYMSNGSVASRLK
AKPALDWNTRKKIAIGAA
RGLFYLHEQCDPKIIHRDVKAA
NILLDEYFEAVVGDFGLAKLLN
HEDSHVTTAVRGTVGHIAPEYL
25 STGQSSEKTDVFGFGILLLELI
TGMRALEFGKSVSQKGAMLEW
VRKLHKEMKVEELVDRELGTTY
DRIEVGEMLQVALLCTQFLPAH
RPKMSEVVQMLE

30

GDGLAERWAASHDHSFYHANM
SYRTITSTDGNNQTKHLFG

SSGFEDEDDNQALDSFAMELSGPR (SEQ ID NO: 47)
35

Arabidopsis thaliana RKS5 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ctagagaattcttataactttttctacg**ATGGAGATT**CTTTGATGAAGTTTCTGTTTTTA
GGAATCTGGGTTTATTATTACTCTGTTCTTACTCTGTTCTGCCATGGATAGTCTTTTA
TCTCCCAAGGTGGCTGCGTTAATGTCAGTGAAGAACAAGATGAAAGATGAGAAAGAGGTT
TTGCTCGGTTGGGATATTAACTCTGTTGATCCTTGACTTGAACATGGTTGGTTGTTCT
TCTGAAGGTTTTGTGGTTTCTCTAGAGATGGCTAGTAAAGGATTATCAGGGATACTATCT
15 ACTAGTATTGGGGAATTAACCTCATCTTCATACTTTGTTACTTCAGAATAATCAGTTAACT
GGTCCGATTCTTCTGAGTTAGGCCAACTCTCTGAGCTTGAAACGCTTGATTATCGGGG
AATCGGTTTAGTGGTGAAATCCCAGCTTCTTTAGGGTTCTTAACCTCACTTAACTACTTG
CGGCTTAGCAGGAATCTTTATCTGGGCAAGTCCCTCACCTCGTCGCTGGCCTCTCAGGT
CTTTCTTTCTTGATCTATCTTTCAACAATCTAAGCGGACCAACTCCGAATATATCAGCA
20 AAAGATTACAGGAAATGCATTTCTTTGTGGTCCAGCTTCCCAAGAGCTTTGCTCAGATGC
TACACCTGTGAGAAATGCTGCAATCGATCTGCAGCGACGGGTTTGTCTGAAAAGGACAAT
AGCAAACATCACAGCTTAGTGCTCTCTTTTGCATTTGGCATTGTTGTTGCCTTTATCATC
TCCCTAATGTTCTCTTCTTCTGGGTGCTTTGGCATCGATCACGTCTCTCAAGATCACAC
GTGCAGCAAGACTACGAATTTGAAATCGGCCATCTGAAAAGGTTCAAGTTTTCGCGAAATA
25 CAAACCGCAACAAGCAATTTTAGTCCAAAGAACATTTTGGGACAAGGAGGGTTTGGGATG
GTTTATAAAGGGTATCTCCCAAATGGAACCTGTGGTGGCAGTTAAAAGATTGAAAGATCCG
ATTTATACAGGAGAAGTTCAGTTTCAAACCGAAGTAGAGATGATTGGCTTAGCTGTTTAC
CGTAACCTTTTACGCCCTCTTTGGATTCTGTATGACCCCGGAAGAGAGAATGCTTGTGTAT
CCGTACATGCCAAATGGAAGCGTAGCTGATCGTCTGAGAGATTGGAATCGGAGGATAAGC
30 ATTGCACTCGGCGCAGCTCGAGGACTTGTTTACTTGCACGAGCAATGCAATCCAAAGATT
ATTCACAGAGACGTCAAAGCTGCAAATATTCTACTTGATGAGAGCTTTGAAGCAATAGTT
GGCGATTTTGGTCTAGCAAAGCTTTTAGACCAGAGAGATTACATGTCACTACCGCAGTC
CGAGGAACCATTTGGACACATCGCTCCCGAGTACCTTTCCACTGGACAGTCTCAGAGAAA
ACCGATGTTTTCGGATTCGGAGTACTAATCCTTGAACCTATAACAGGTATAAGATGATT
35 GATCAAGGCAATGGTCAAGTTCGAAAAGGAATGATATTGAGCTGGGTAAGGACATTGAAA
GCAGAGAAGAGATTTGCAGAGATGGTGGACAGAGATTTGAAGGGAGAGTTTGATGATTTG
GTGTTGGAGGAAGTAGTGAATTGGCTTTGCTTTGTACACAGCCACATCCGAATCTAAGA
CCGAGGATGTCTCAAGTGTGAAGGTACTAGAAGGTTTAGTGGAACAGTGTGAAGGAGGG
TATGAAGCTAGAGCTCCAAGTGTCTCTAGGAACTACAGTAATGGTCATGAAGAGCAGTCC
40 TTTATTATTGAAGCCATTGAGCTCTCTGGACCACGATGAtagacttcatagtgtcttaac

tagtcttcttgattttgttgatgtcatggc (SEQ ID NO: 48)

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS5 protein.

- 5 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).
- At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains no
- 10 leucine zipper motif, in contrast to the other RKS proteins. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues.
- 15 The fifth domain contains many serine residues, and is likely to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine /
- 20 threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein /
- 25 protein interactions.

MEISLMKFLEFLGIWVYYYS

VLDSVSAMDSLLSPKV

30

AALMSVKNMKDE

KEVLSGWDINSVD

PCTWNNMVGCSSEGFVVS

35

LEMASKGLSGILS

T SIGELTHLHTLLQNNQLTGPI

PSELGQLSELETLDLSGNRFSGEI

PASLGFLTHLNYLRLSRNLLSGQV

PHLVAGLSGLSFLDLSFNLSGPT
PNISAK DYRKCISLWSSFPR

ALLRCYTCEKCCNR
5 SAATGLSEKDNSK

HHSLVLSFAFGIVV
AFIISLMFLFFWVLWH

10 RSRLSRSHVQQDYEF
EIGHLKRFSFREIQTAT

SNFSPKNILQGGFGMVYKGYLPN
GTVVAVKRLKDPIYTGEVQFQ
15 TEVEMIGLAVHRNLLRLFGFCM
TPEERMLVYPMPNGSVADRLR
DWNRRISIALGAA
RGLVYLHEQCNPKIIHRDVKAA
NILLDESFEAIVGDFGLAKLLD
20 QRDSHVTTAVRGTTIGHIAPEYL
STGQSSEKTDVFGFVLELELI
TGHKMIDQNGQVRKGMILSW
VRTLKAEKRAEMVDRDLKGEF
DDLVL EEVVELALLCTQPHPNL
25 RPRMSQVLKV

LEGLVEQCEGGYEARA

PASVSRNYSNGHEEQSFIIIEAIELSGPR (SEQ ID NO: 49)
30

Arabidopsis thaliana RKS6 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

```
attgtttccttcttttgggattttctccttggatggaaccagctcaattaatgagatgag
10 ATGGAGAATGTTCAGCTTGCAGAAGATGGCTATGGCTTTTACTCTCTTGTTTTTGCCTGT
TTATGCTCATTGTGTCTCCAGATGCTCAAGGGGATGCACTGTTTGCCTTGAGGATCTCC
TTACGTGCATTACCGAATCAGCTAAGTGACTGGAATCAGAACCAAGTTAATCCTTGCACT
TGGTCCCAAGTTATTTGTGATGACAAAACTTTGTCACTTCTCTTACATTGTCAGATATG
AACTTCTCGGGAACCTTGCTTCAAGAGTAGGAATCCTAGAAAATCTCAAGACTCTTACT
15 TTAAAGGGAAATGGAATTACGGGTGAAATACCAGAAGACTTTGGAAATCTGACTAGCTTG
ACTAGTTTGGATTGGAGGACAATCAGCTAACTGGTCGTATACCATCCACTATCGGTAAT
CTCAAGAAACTTCAGTTCTTGACCTTGAGTAGGAACAACTTAATGGGACTATTCCGGAG
TCACTCACTGGTCTTCCAAACCTGTTAAACCTGCTGCTTGATTCCAATAGTCTCAGTGGT
CAGATTCTCAAAGTCTGTTTGAGATCCCAAAATATAATTCACGTCAAACAACTTGAAT
20 TGTGGCGGTCGTC AACCTCACCCTTGTGTATCCGCGGTTGCCCATTCAGGTGATTCAAGC
AAGCCTAAAACTGGCATTATTGCTGGAGTTGTTGCTGGAGTTACAGTTGTTCTCTTTGGA
ATCTTGTTGTTTCTGTTCTGCAAGGATAGGCATAAAGGATATAGACGTGATGTGTTTG
GATGTTGCAGGTGAAGTGGACAGGAGAATTGCATTTGGACAGTTGAAAAGGTTTGCATGG
AGAGAGCTCCAGTTAGCGACAGATAACTTCAGCGAAAAGAATGTACTTGGTCAAGGAGGC
25 TTTGGGAAAGTTTACAAAGGAGTGCTTCCGGATACACCCAAAGTTGCTGTGAAGAGATTG
ACGGATTTCGAAAGTCCTGGTGGAGATGCTGCTTCCAAAGGGAAGTAGAGATGATAAGT
GTAGCTGTTTCATAGGAATCTACTCCGTCTTATCGGGTTCTGCACCACACAAACAGAACGC
CTTTTGGTTTATCCCTTCATGCAGAATCTAAGTCTTGACATCGTCTGAGAGAGATCAAA
GCAGGCGACCCGGTTCTAGATTGGGAGACGAGGAAACGGATTGCCCTTAGGAGCAGCGCGT
30 GGTTTTGAGTATCTTCATGAACATTGCAATCCGAAGATCATACTCGTGATGTGAAAGCA
GCTAATGTGTTACTAGATGAAGATTTTGAAGCAGTGTTGGTGATTTTGGTTTAGCCAAG
CTAGTAGATGTTAGAAGGACTAATGTGACTACTCAAGTTCGAGGAACAATGGGTCACATT
GCACCAGAATATTTATCAACAGGGAAATCATCAGAGAGAACCGATGTTTTCGGGTATGGA
ATTATGCTTCTTGAGCTTGTTACAGGACAACCGCAATAGACTTTTTCAGGTTTGGAGGAA
35 GAAGATGATGTCTTGTTACTTGACCACGTGAAGAACTGGAAAGAGAGAAGAGATTAGGA
GCAATCGTAGATAAGAATTTGGATGGAGAGTATATAAAGAAGAAGTAGAGATGATGATA
CAAGTGGCTTTGCTTTGTACACAAGGTTCAACAGAAGACCGACAGTGATGTCTGAAGTT
GTGAGGATGTTAGAAGGAGAAGGGCTTGCAGGAGAGATGGGAAGAGTGGCAAAACGTGGAA
GTCACGAGACGTCATGAGTTTGAACGGTTGCAGAGGAGATTTGATTGGGGTGAAGATTCT
40 ATGCATAACCAAGATGCCATTGAATTATCTGGTGAAGATGAccaaaaacatcaaacctt (SEQ ID NO: 50)
```

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS6 protein.

Different domains are spaced and shown from the N-terminus
5 towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each
10 separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain
15 contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown
20 function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single
25 leucine rich repeat, probably involved in protein / protein interactions.

MRMFSL

QKMAMAF TLLFFACLCSFVSPDAQG

30

DALFALRISLRALP

NQLSDWNQNQVN

PCTWSQVICDDKNEVTSL

35

TLSDMNFSGTLSSRV

GILENLKTLTLKNGITGEI

PEDFGNLTSLTSLDLEDNQLTGRI

PSTIGNLKKLQFLTLNRKLNGTI
PESLTGLPNLLNLLDLSNLSGQI
PQSLFEIPKYNFTSNNLNCGG

5 RQPHPCVSAVAHSGDSSKPKTG

IIAGVVAGVTVVL
FGILLEFLFC

10 KDRHKGYYRDRVFDVAGE
VDRRIAFGQLKRFARRELQIAT

DNFSEKNVLGQGGFGKVYKGVLPD
TPKVAVKRLTDFESPGDAAFQ
15 REDEMISVAVHRNLLRLIGFCT
TQTERLLVYPFMQNLSLAHRLR
EIKAGDPVLDWETRKRIALGAA
RGFEYLHEHCNPKIIHRDVKAA
NVLLDEDFEAVVGDFGLAKLVD

20 VRRTNVTTQVRGTMGHIAPEYL
STGKSSERTDVFYGYIMLLELV
TGQRAIDFSRLEEEDDVLLLDH
VKKLEREKRLGAIVDKNLDGEY
IKKEVEMMIQVALLCTQGSPE

25 RPVMSEVVRMLE

GEGLAERWEWQNVETRRHEFE

RLQRRFDWGEDSMHNQDAIELSGGR (SEQ ID NO: 51)

30

Arabidopsis thaliana RKS7 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 acatccttgttttctgctcattcctctgtttcaaca**ATGG**AGAGTACTATTGTTATGATGA
TGATGATAACAAGATCTTTCTTTTGCTTCTTGGGATTTTATGCCTTCTCTGCTCTTCTG
TTCACGGATTGCTTTCTCCTAAAGGTGTTAACTTTGAAGTGAAGCTTTGATGGACATAA
AAGCTTCATTACATGATCCTCATGGTGTCTTGATAACTGGGATAGAGATGCTGTTGATC
CTTGTAGTTGGACAATGGTCACTTGTCTTCTGAAAACCTTTGTCATTGGCTTAGGCACAC
15 CAAGTCAGAATTTATCTGGTACACTATCTCCAAGCATTACCAACTTAACAAATCTTCGGA
TTGTGCTGTTGCAGAACAAACATAAAAGGAAAAATTCCTGCTGAGATTGGTCGGCTTA
CGAGGCTTGAGACTCTTGATCTTTCTGATAATTTCTTCCACGGTGAAATTCCTTTTTCAG
TAGGCTATCTACAAAGCCTGCAATATCTGAGGCTTAACAACAATTCTCTCTCTGGAGTGT
TTCCTCTGTCACTATCTAATATGACTCAACTTGCCTTTCTTGATTTATCATAACAACATC
20 TTAGTGGTCCTGTTCCAAGATTTGCTGCAAAGACGTTTAGCATCGTTGGGAACCCGCTGA
TATGTCCAACGGGTACCGAACAGACTGCAATGGAACAACATTGATACCTATGTCTATGA
ACTTGAATCAAACCTGGAGTTCCTTTATACGCCGGTGGATCGAGGAATCACAAAATGGCAA
TCGCTGTTGGATCCAGCGTTGGGACTGTATCATTAATCTTCATTGCTGTTGGTTTGTTC
TCTGGTGGAGACAAAGACATAACCAAAACACATTCTTTGATGTTAAAGATGGGAATCATC
25 ATGAGGAAGTTTCACTTGGAAACCTGAGGAGATTGGTTTCAGGGAGCTTCAGATTGCGA
CCAATAACTTCAGCAGTAAGAACTTATGGGGAAAGGTGGCTATGGAAATGTATACAAAG
GAATACTTGGAGATAGTACAGTGGTTCAGTGAAGGCTTAAAGATGGAGGAGCATTGG
GAGGAGAGATTCACTTTCAGACAGAAGTTGAAATGATCAGTTTAGCTGTTATCGAAATC
TCTTAAGACTCTACGGTTTCTGCATCACACAACTGAGAAGCTTCTAGTTTATCCTTATA
30 TGTCTAATGGAAGCGTTGCATCTCGAATGAAAGCAAAACCTGTTCTTGACTGGAGCATAA
GGAAGAGGATAGCCATAGGAGCTGCAAGAGGGCTTGTGTATCTCCATGAGCAATGTGATC
CGAAGATTATCCACCGGATGTCAAAGCAGCGAATATACTTCTTGATGACTACTGTGAAG
CTGTGGTTGGCGATTTTGGTTTAGCTAAACTCTTGATCATCAAGATTCTCATGTGACAA
CCGCGGTTAGAGGCACGGTGGGTACATTGCTCCAGAGTATCTCTCAACTGGTCAATCCT
35 CTGAGAAAACAGATGTTTTTGGCTTCGGGATTCCTTCTTCTTGAGCTTGTAACCGGACAAA
GAGCTTTTGAGTTTGGTAAAGCGGCTAACGAGAAAGGTGTGATGCTTGATTGGGTAAAAA
AGATTCATCAAGAGAAGAACTTGAGCTACTTGTGGATAAAGAGTTGTTGAAGAAGAAGA
GCTACGATGAGATTGAGTTAGACGAAATGGTAAGAGTAGCTTTGTTGTGCACACAGTACC
TGCCAGGACATAGACCAAAAATGTCTGAAGTTGTTCAATGCTGGAAGGAGATGGACTTG
40 CAGAGAAATGGGAAGCTTCTCAAAGATCAGACAGTGTTCAAAATGTAGCAACAGGATAA

ATGAATTGATGTCATCTTCAGACAGATACTCTGATCTTACCGATGACTCTAGTTTACTTG
TGCAAGCAATGGAGCTCTCTGGTCCTAGATGAaatctatacatgaatctgaagaagaaga
agaacatgcatctgtttcttgaatcaagagggattctgtttttttgtataatagagagg
ttttttggagggaaatgttgtgtctctgttaactgtataggcttgttgtgaagaagttat
5 tactgcacttagggtaattcaaagttctttacataaaaaatgattagttgcgttgaata
gaggggaacactttgggagatttcatgtatgaaatttggaaaaaaaaaaaaaaaaaa (SEQ ID NO: 52)

10 Predicted amino acid sequence of the *Arabidopsis thaliana* RKS7 protein.

Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al (1997).

15 At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 3 leucine residues, each separated by seven other amino acids. The third domain contains conserved cysteine residues, involved in disulphate
20 bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline residues, and to be a site for O-
25 glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably
30 also containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

35

MESTIVMMMITRSFF
CFLGFLCCLCSSVHGLLSPKGVNFEV

QALMDIKASLHDP
HGVLDNWDRDAVD

5 PCSWTMVTCSSENFVIG

LGTFSQNLSGTL
SPSITNLTLNRIVLLQNNNIKGKI
PAEIGRLTRLETLDLSDNFFHGEI
PFSVGYLQSLQYLRLNNSLSGVF
10 PLSLSNMTQLAFLDLSYNNLSGPV
PRFAA KTFISIVGNPLICPT

GTEPDCNGTTLIPMSMNL
NQTGVPLYAGGSRNHKMA
15
IAVGSSVGTVSLIFIAVGLEFLWW

RQRHNQNTFFDVKDGHNHHE
EVSLGNLRRFGFRELQIAT
20
NNFSSKNLLGKGGYGNVYKGILGD
STVVAVKRLKDGGALGGEIQFQ
TEVEMISLAVHRNLLRLYGFCI
TQTEKLLVYPYMSNGSVA
25 SRMKAKPVLDSIRKRIAIGAA
RGLVYLHEQCDPKIIHRDVKAA
NILLDDYCEAVVGDFGLAKLLD
HQDSHVTTAVRGTVGHIAPEYL
STGQSSEKTDVFGFGILLLELV
30 TGQRAFEFGKAANQKGVMLDW
VKKIHQEKKLELLVDKELLKKKSY
DEIELDEMVRVALLCTQYLPGH
RPKMSEVVRMLE

35 GDGLAEKWEASQRSDS
VSKCSNRINELMSSS

DRYSDLTDDSSLLVQAMELSGPR (SEQ ID NO: 53)

Arabidopsis thaliana RKS8 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 gttttttttttttaccctcttgaggatctgggaggagaaatttgcttttttttggttaa
ATGGGGAGAAAAAGTTGAAGCTTTTGGTTTGTCTGCTTAATCTCACTGCTTCTTCTG
TTTAATTCGTTATGGCTTGCCTCTTCTAACATGGAAGGTGATGCACTGCACAGTTTGAGA
GCTAATCTAGTTGATCCAAATAATGTCTTGCAAAGCTGGGATCCTACGCTTGTTAATCCG
TGTACTTGGTTTTCAGTAACGTGTAACAACGAGAACAGTGTTATAAGAGTCGATCTTGGG
15 AATGCAGACTTGTCTGGTCAGTTGGTTCCCTCAGCTAGGTCAGCTCAAGAACTTGCAGTAC
TTGGAGCTTTATAGTAATAACATAACCGGGCCGGTCCAAGCGATCTTGGGAATCTGACA
AACTTAGTGAGCTTGGATCTTTACTTGAACAGCTTCACTGGTCCAATTCCAGATTCTCTA
GGAAAGCTATTCAAGCTTCGC'TTCTTCGGCTCAACAATAACAGTCTCACCGGACCAATT
CCCATGTCATTGACTAATATCATGACCC'TTCAAGTTTGGATCTGTGCAACAACCGATTA
20 TCCGGATCTGTTCC'TGATAATGGTTCC'TTCTCGCTCTTCACTCCCATCAGTTT'TGCTAAC
AACTTGGATCTATGCGGCCAGTTACTAGCCGTCCTTGTCTGGATCTCCCCGTTT'TCT
CCTCCACCACCTTTTATACCACCTCCCATAGTTCC'TACACCAGGTGGGTATAGTGCTACT
GGAGCCATTGCGGGAGGAGTTGCTGCTGGTGCTGCTTACTATT'TGCTGCCCC'TGCTT'A
GCTTTT'GCTTGGTGGCGTAGAAGAAACCTCAAGAATTCTTCTTTGATGTTCTCGCCGAA
25 GAGGACCCTGAGGTTCACTTGGGGCAGCTTAAGCGGTTCTCTCTACGGGAAC'TTCAAGTA
GCAACTGATAGCTTCAGCAACAAGAACATTTTGGGCCGAGGTGGGTTTCGAAAAGTCTAC
AAAGCCGCTCTTGCTGATGGAACACTTGTGTCAGTCAAACGGCTTAAAGAAGAGCGAACC
CCAGGTGGCGAGCTCCAGTTTCAGACAGAAGTGGAGATGATAAGCATGGCCGTTACAGA
AATCTCCTCAGGCTACGCGGTTTCTGTATGACCCCTACCGAGAGATTGCTTGT'TATCCT
30 TACATGGCTAATGGAAGTGTGCTTCC'TGTTT'GAGAGAACGTCCACCATCACAGTTGCCT
CTAGCCTGGTCAATAAGACAGCAAATCGCGCTAGGATCAGCGAGGGGTTTGTCTTATCTT
CATGATCATTGCGACCCCAAATATTCACCGTGATGTGAAAGCTGCTAATATTCTGTTG
GACGAGGAATTTGAGGCGGTGGTAGGTGATTT'CGGGTTAGCTAGACTTATGGACTATAAA
GATACTCATGTCAACGGCTGTGCGTGGGACTATTGGACACATTGCTCCTGAGTATCTC
35 TCAACTGGAAAATCTTCAGAGAAAAGTATGTTTTTGGCTACGGGATCATGCTTTTGGAA
CTGATTACAGGTCAGAGAGCTTTT'GATCTTGCAAGACTGGCGAATGACGATGACGTTATG
CTCCTAGATTGGGTGAAAGGGCTTTTGAAGGAGAAGAAGCTGGAGATGCTTGTGGATCCT
GACCTGCAAAGCAATTACACAGAAGCAGAAGTAGAACAGCTCATACAAGTGGCTCTTCTC
TGCACACAGAGCTCACCTATGGAACGACCTAAGATGTCTGAGGTTGTTCGAATGCTTGAA
40 GGTGACGGTTTAGCGGAGAAATGGGACGAGTGGCAGAAAGTGGAAGTTCTCAGGCAAGAA

GTGGAGCTCTCTTCTACCCACCTCTGACTGGATCCTTGATTGACTGATAATCTTCAT
GCTATGGAGTTGTCTGGTCCAAGATAAacgacattgtaatttgccaaacagaaaagagaa
agaacagagaaaattaagagaatcacttctctgtattctt (SEQ ID NO: 54)

5

Predicted amino acid sequence of the *Arabidopsis thaliana* RKS8 protein.

10 Different domains are spaced and shown from the N-terminus towards the C-terminus. Overall domain structure is similar as described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain represents a signal sequence. The second domain contains a leucine zipper motif, containing 4 leucine residues, each separated by seven other amino
15 acids. The third domain contains conserved cysteine residues, involved in disulphate bridge formation. The fourth domain contains a leucine rich repeat domain, consisting of 5 complete repeats of each approximately 24 amino acid residues. The fifth domain contains many serine and proline residues, and is likely to contain hydroxy-proline
20 residues, and to be a site for O-glycosylation. The sixth domain contains a single transmembrane domain after which the predicted intracellular domains are positioned. The seventh domain has an unknown function. The eighth domain represents a serine / threonine protein kinase domain (Schmidt et al. 1997) and is probably also
25 containing sequences for protein / protein interactions. The ninth domain has an unknown function. The last and tenth domain at the C-terminal end represents part of a single leucine rich repeat, probably involved in protein / protein interactions.

30 MGRKKFEAFGVCLISLLLLFNSL
WLASSNMEG

DALHSLRANLVDP
NNVLQSWDPTLVN

35

PCTWFHVTCNNNSVIRV

DLGNADLSGQLV

P QLGQLKNLQYLELYSNNITGPV

40 PSDLGNLTNLVSLDLYLNSFTGPI

PDSLGLKLFKLRFLRLNNSLTGPI
PMSLTNIMTLQVLDLSNNRLSGSV
PDNGSFSLFTPISFANNLDLCGPV

5 TSRPCPGSPPFSPPPP
 FIPPPIVPTPGGYSATG

AIAGGVAAGAAL
LFAAPALAFWW

10 RRRKPOEFFFDVPAEEDPE
 VHLGQLKRFSLRELQVAT

DSFSNKNILGRGGFGKVYKGRAD
15 GTLVAVKRLKEERTPGGELQFQ
 TEVEMISMAVHRNLLRLRGFCM
 TPTERLLVYPYMANGSVASCLR
 ERPPSQLPLAWSIRQQIALGSA
 RGLSYLHDHCDPKIIHRDVKAA

20 NILLDEEFEAVVGDFGLARLMD
 YKDTHVTTAVRGITIGHIAPEYL
 STGKSSEKTDVFGYGIMLLELI
 TGQRAFDLARLANDDDVMLLDW
 VKGLLKEKKLEMLVDPDLQSNY

25 TEAEVEQLIQVALLCTQSSPME
 RPKMSEVVRMLE

GDGLAEKWDEWQKVEVLRQEVLS

30 SHPTSDWILDSTDNLHAMELSGPR (SEQ ID NO: 55)

Arabidopsis thaliana rks10 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 atcagggggttttaacaatgatggatctctctgatgagggatagttctagggttggttt
taatctcttgaggataaaa**ATGGAACGAAGATTAATGATCCCTTGCTTCTTTTGGTTGATT**
CTCGTTTTGGATTGGTTCTCAGAGTCTCGGGCAACGCCGAAGGTGATGCTCTAAGTGCA
CTGAAAAACAGTTTAGCCGACCCTAATAAGGTGCTTCAAAGTTGGGATGCTACTCTTGTT
ACTCCATGTACATGGTTTTCATGTTACTTGCAATAGCGACAATAGTGTACACGTGTGAC
15 CTTGGGAATGCAAATCTATCTGGACAGCTCGTAATGCAACTTGGTCAGCTTCCAACTTG
CAGTACTTGGAGCTTTATAGCAATAACATTACTGGGACAATCCCAGAACAGCTTGGAAAT
CTGACGGAATTGGTGAGCTTGGATCTTACTTGAACAATTTAAGCGGGCCTATTCCATCA
ACTCTCGGCCGACTTAAGAACTCCGTTTCTTGCCTCTTAATAACAATAGCTTATCTGGA
GAAATTCGAAGTCTTTGACTGCTGTCTGACGCTACAAGTTCTGGATCTCTCAAACAAT
20 CCTCTCACCGGAGATATTCCTGTTAATGGTTCCTTTTCACTTTTCACTCCAATCAGTTTT
GCCAACACCAAGTTGACTCCCCCTTCTGCATCTCCACCGCCTCTATCTCTCTACACCG
CCATCACCTGCAGGGAGTAATAGAATTACTGGAGCGATTGCGGGAGGAGTTGCTGCAGGT
GCTGCACTTCTATTTGCTGTTCCGGCCATTGCACTAGCTTGGTGGCGAAGGAAAAAGCCG
CAGGACCACTTCTTTGATGTACCAGCTGAAGAGGACCCAGAAGTTCATTTAGGACAACCTG
25 AAGAGGTTTTTCATTGCGTGAACACTACAAGTTGCTTCGGATAATTTTAGCAACAAGAACATA
TTGGGTAGAGGTGGTTTTGGTAAAGTTTATAAAGGACGGTTAGCTGATGGTACTTTAGTG
GCCGTTAAAAGGCTAAAAGAGGAGCGCACCAAGGTGGCGAACTGCAGTTCAGACAGAG
GTTGAGATGATTAGTATGGCGGTTACAGAACTTGCTTCGGCTTCGTGGATTTTGCATG
ACTCCAACCGAAAGATTGCTTGTTTATCCCTACATGGCTAATGGAAGTGTGCCTCCTGT
30 TTAAGAGAACGTCCCGAGTCCCAGCCACCACTTGATTGGCCAAAGAGACAGCGTATTGCG
TTGGGATCTGCAAGAGGGCTTGCGTATTTACATGATCATTGCGACCCAAAGATTATTCAT
CGAGATGTGAAAGCTGCAAAATATTTTGTGGATGAAGAGTTTGAAGCCGTGGTTGGGGAT
TTTGGACTTGCAAACTCATGGACTACAAAGACACACATGTGACAACCGCAGTGCCTGGG
ACAAATTGGTCATATAGCCCCTGAGTACCTTTCCACTGGAAAATCATCAGAGAAAACCGAT
35 GTCTTTGGGTATGGAGTCATGCTTCTTGAGCTTATCACTGGACAAAGGGCTTTTGATCTT
GCTCGCCTCGCGAATGATGATGATGTGATGTTACTAGACTGGGTGAAAGGGTTGTTAAAA
GAGAAGAAATTGGAAGCACTAGTAGATGTTGATCTTCAGGGTAATTACAAAGACGAAGAA
GTGGAGCAGCTAATCCAAGTGGCTTTACTCTGCACTCAGAGTTCACCAATGGAAAGACCC
AAAATGTCTGAAGTTGTAAGAATGCTTGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAG
40 TGGCAAAAGGAGGAAATGTTGAGACAAGATTTCAACTACCCAACCCACCATCCAGCCGTG

TCTGGCTGGATCATTGGCGATTCCACTTCCCAGATCGAAAACGAATACCCCTCGGGTCCA
AGATAAagattcgaaacacgaatgttttttctgtattttgttttctctgtatttattgag
ggttttagcttc (SEQ ID NO: 56)

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS10 protein.

Different domains are spaced and shown from the N-terminus
10 towards the C-terminus. Overall domain structure is similar as
described in Schmidt et al. (1997).
At the predicted extracellular domain the first domain represents a
signal sequence. The second domain contains a leucine zipper motif,
containing 4 leucine residues, each separated by seven other amino
15 acids. The third domain contains conserved cysteine residues,
involved in disulphate bridge formation. The fourth domain contains a
leucine rich repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain contains many
serine and proline residues, and is likely to contain hydroxy-proline
20 residues, and to be a site for O-glycosylation. The sixth domain
contains a single transmembrane domain after which the predicted
intracellular domains are positioned. The seventh domain has an
unknown function. The eighth domain represents a serine / threonine
protein kinase domain (Schmidt et al. 1997) and is probably also
25 containing sequences for protein / protein interactions. The ninth
domain has an unknown function. The last and tenth domain at the C-
terminal end represents part of a single leucine rich repeat,
probably involved in protein / protein interactions.

30 MERRLMIPCFFWLILVL
DLVLRVSGNAEG

DALSALKNSLADP
NKVLQSWDATLVT

35 PCTWFHVTCSNDSVTRV

DLGNANLSGQLV
M QLGQLPNLQYLELYSNNITGTI
40 PEQLGNLTELVS LDLYLNNLSGPI

PSTLGRLKKLRFLRLNNNSLSGEI
PRSLTAVLTQLQVLDLSNNPLTGDI
PVNGSFSLTPISFANTK LT PL

5 PASPPPPISPTPPSPAGSNRITG

AIAGGVAAGAAL
LFAVPAIALAWW

10 RRKKPQDHFFDVPAEEDPE
VHLGQLKRFSLRELQVAS

DNFSNKNILGRGGFGKVYKGRLAD
GTLVAVKRLKEERTQGGELOFQ
15 TEVEMISMAVHRNLLRLRGFCM
TPTERLLVYPYMANGSVASCLR
ERPESQPPLDWPKRQRIALGSA
RGLAYLHDHCDPKIIHRDVKAA
NILLDEEFEAVVGDFGLAKLMD
20 YKDTHTTAVRGTIGHIAPEYL
STGKSSEKTDVFGYGVMLLELI
TGQRAFDLARLANDDDVMLLDW
VKGLLKEKKLEALVDVDLQGNV
KDEEVEQLIQVALLCTQSSPME
25 RPKMSEVVRMLE

GDGLAERWEEWQKEEMFRQDFNYPTHH

PAVSGWIIGDSTSQIENEYPSGPR (SEQ ID NO: 57)

Arabidopsis thaliana RKS 11 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ttgttaacctctcgttaactaaaatcttcc**ATGG**TAGTAGTAACAAAGAAGACCATGAAGA
TTCAAATTCATCTCCTTTACTCGTTCTTGTTCTCTCTACTCTCACTCTATCTT
CTGAGCCCAGAAACCTGAAGTTGAGGCGTTGATAAGTATAAGGAACAATTTGCATGATC
CTCATGGAGCTTTGAACAATTGGGACGAGTTTTCAGTTGATCCTTGAGCTGGGCTATGA
TCACTTGCTCTCCCGACAACCTCGTCATTGGACTAGGAGCGCCGAGCCAGTCTCTCTCGG
15 GAGGTTTATCTGAGTCTATCGGAAATCTCACAATCTCCGACAAGTGTCATTGCAAAATA
ACAACATCTCCGGCAAAATCCACCGGAGCTCGGTTTTCTACCCAAATTACAAACCTTGG
ATCTTTCCAACAACCGATTCTCCGGTGACATCCCTGTTTCCATCGACCAGCTAAGCAGCC
TTCAATATCTGAGACTCAACAACAACCTCTTTGTCTGGGCCCTTCCCTGCTTCTTTGTCCC
AAATTCCTCACCTCTCCTTCTTGACTTGCTTTACAACAATCTCAGTGGCCCTGTTCCCTA
20 AATTCACGCAAGGACTTTAAACGTTGCTGGTAATCCTTTGATTGTAGAAGCAACCCAC
CTGAGATTTGTTCTGGATCAATCAATGCAAGTCCACTTTCTGTTTCTTTGAGCTCTTCAT
CAGGACGCAGGTCTAATAGATTGGCAATAGCTCTTAGTGTAAGCCTTGGCTCTGTTGTTA
TACTAGTCCTTGCTCTCGGGTCCTTTTGTGTTGTAACGAAAGAAACAAAGAAGGCTACTGA
TCCTTAACTTAAACGCAGATAAACAAGAGGAAGGGCTTCAAGGACTTGGGAATCTAAGAA
25 GCTTCACATTCAAGAACTCCATGTTTATACAGATGGTTTCAGTTCCAAGAACATTCTCG
GCGCTGGTGGATTCCGTAATGTGTACAGAGGCAAGCTTGGAGATGGGACAATGGTGGCAG
TGAAACGGTTGAAGGATATTAATGGAACCTCAGGGGATTCACAGTTTCGTATGGAGCTAG
AGATGATTAGCTTAGCTGTTCAAGAATCTGCTTCGGTTAATGGTTATTGCGCAACTT
CTGGTGAAAGGCTTCTTGTTTACCCCTACATGCCCTAATGGAAGCGTCGCCTCTAAGCTTA
30 AATCTAAACCGGCATTGGACTGGAACATGAGGAAGAGGATAGCAATTGGTGCAGCGAGAG
GTTTGTGTATCTACATGAGCAATGTGATCCCAAGATCATTCATAGAGATGTAAAGGCAG
CTAATATTCTCTTAGACGAGTGCTTTGAAGCTGTTGTTGGTGACTTTGGACTCGCAAAGC
TCCTTAACCATGCGGATTCTCATGTCACAACTGCGGTCCGTGGTACGGTTGGCCACATTG
CACCTGAATATCTCTCCACTGGTCAGTCTTCTGAGAAAACCGATGTGTTTGGGTTCGGTA
35 TACTATTGCTCGAGCTCATAACCGGACTGAGAGCTCTTGAGTTTGGTAAAACGTTAGCC
AGAAAGGAGCTATGCTTGAATGGGTGAGGAAATTACATGAAGAGATGAAAGTAGAGGAAC
TATTGGATCGAGAACTCGGAATAACTACGATAAGATTGAAGTTGGAGAGATGTTGCAAG
TGGCTTTGCTATGCACACAATATCTGCCAGCTCATCGTCTAAAATGTCTGAAGTTGTTT
TGATGCTTGAAGGCGATGGATTAGCCGAGAGATGGGCTGCTTCGCATAACCATTACATT
40 TCTACCATGCCAATATCTCTTCAAGACAATCTCTTCTGTCTACTACTTCTGTCTCAA

GGCTTGACGCACATTGCAATGATCCAACCTTATCAAATGTTTGGATCTTCGGCTTTCGATG
ATGACGATGATCATCAGCCTTTAGATTCTTTGCCATGGAACCTATCCGGTCCAAGATAAc
acaatgaaagaaagatatcattttttacgatggatcaaacaatccaatgaaaaaa (SEQ ID NO: 58)

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS11 protein.

10 Different domains are spaced and shown from the N-terminus
towards the C-terminus. Overall domain structure is similar as
described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains a
15 leucine zipper motif, containing 3 leucine residues, each
separated by seven other amino acids. The third domain
contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
20 approximately 24 amino acid residues. The fifth domain
contains many serine and proline residues, and is likely to
contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
25 domains are positioned. The seventh domain has an unknown
function. The eight domain represents a serine / threonine
protein kinase domain (Schmidt et al. 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
30 domain at the C-terminal end represents part of a single
leucine rich repeat, probably involved in protein / protein
interactions.

MVVVTKKTMKIQIHLLYSFLFL
35 CFSTLTLSSEPRNPEV

EALISIRNNLHDP
HGALNNWDEFSVD

PCSWAMITCSPDNLVIGL

GAPSQSLSGGLS

5 ESIGNLTNLRQVSLQNNISGKI
PPELGFLPKLQTLDLSENRFSGDI
PVSIDQLSSLQYLRLNNSLSGPF
PASLSQIPHLSFLDLSYNNLSGPV
PKFPARTFNVAGNPLICRSN

10 PPEICSGSINASPL
SVSLSSSSGRRSNR

LAIALSVSLGSVVIL
15 VLALGSFCWY

RKKQRRLLILNLNGADKQEE
GLQGLGNLRSFTFRELHVYT

20 DGFSSKNILGAGGFGNVYRGKLG
GTMVAVKRLKDINGTSGDSQFR
MELEMISLAVHKNNLLRLIGYCA
TSGERLLVYPMPNGSVASKLK
SKPALDWNMRKRIAIGAA

25 RGLLYLHEQCDPKIIHRDVKAA
NILLDECFEAVVGDFGLAKLLN
HADSHVTTAVRGTVGHIAPEYL
STGQSSEKTDVFGFGILLLELI
TGLRALEFGKTVSOKGAMLEW

30 VRKLHEEMKVEELLDRELGTNY
DKIEVGEMLQVALLCTQYLPAA
RPKMSEVVLMLE

GDGLAERWAASHNHSHFYHANI
35 SFKTISSLSTTSVSRDLAHCNDPTYQMFG

SSAFDDDDHQPLDSFAMELSGPR (SEQ ID NO: 59)

Arabidopsis thaliana RKS12 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 tttaaaaaccttgctagttctcaattctcatgactttgcttttagtcttagaagtggaaa
ATGGAACATGGATCATCCCGTGGCTTTATTTGGCTGATTCTATTTCTCGATTTTGTTC
AGAGTCACCGGAAAAACACAAGTTGATGCTCTCATTGCTCTAAGAAGCAGTTTATCATCA
GGTGACCATACAAACAATATACTCCAAAGCTGGAATGCCACTCACGTTACTCCATGTTCA
TGGTTTCATGTTACTTGCAATACTGAAAACAGTGTTACTCGTCTTGACCTGGGGAGTGCT
15 AATCTATCTGGAGAACTGGTGCCACAGCTTGCTCAGCTTCCAAATTTGCAGTACTTGGAA
CTTTTAAACAATAATATTACTGGGGAGATACCTGAGGAGCTTGGCGACTTGATGGAATA
GTAAGCTTGGACCTTTTTGCAAACAACATAAGCGGTCCCATCCCTTCTCTTGGCAAA
CTAGGAAAACCTCCGCTTCTTGCGTCTTTATAACAACAGCTTATCTGGAGAAATCCAAGG
TCTTTGACTGCTCTGCCGCTGGATGTTCTTGATATCTCAAACAATCGGCTCAGTGGAGAT
20 ATTCTGTTAATGGTTCCCTTTTCGCAGTTCACCTTCTATGAGTTTGGCAATAATAAATTA
AGGCCGCGACCTGCATCTCCTTCACCATCACCTTCAGGAACGCTGTCAGCAATAGTAGTG
GGAGTTGCTGCGGGTGCACTTCTATTTGCGCTTGCTTGGTGGCTGAGAAGAAAACCTG
CAGGGTCACCTTTCTTGATGTACCTGCTGAAGAAGACCCAGAGGTTTATTTAGGACAATTT
AAAAGGTTCTCCTTGCGTGAAGTGTAGTTGCTACAGAGAAATTTAGCAAAAGAAATGTA
25 TTGGGCAAAGGACGTTTTTGGTATATTGTATAAAGGACGTTTAGCTGATGACACTCTAGTG
GCTGTGAAACGGCTAAATGAAGAACGTACCAAGGGTGGGGAACGTCAGTTTCAAACCGAA
GTTGAGATGATCAGTATGGCCGTTTCATAGGAACCTGCTTCGGCTTCGTGGCTTTTGCAATG
ACTCCAAGTGAAGATTACTTGTATCCCTACATGGCTAATGGAAGTGTGCTTCTTGT
TTAAGAGAGCGTCCTGAAGGCAATCCAGCCCTTGACTGGCCAAAAGAAAGCATATTGCT
30 CTGGGATCAGCAAGGGGGCTCGCATATTTACACGATCATTGCGACCAAAGATCATTAC
CTGGATGTGAAAGCTGCAATATACTGTTAGATGAAGAGTTTGAAGCTGTTGTTGGAGAT
TTTGGGCTAGCAAAATTAATGAATTATAACGACTCCCATGTGACAACTGCTGTACGGGGT
ACGATTGGCCATATAGCGCCGAGTACCTCTCGACAGGAAATCTTCTGAGAAGACTGAT
GTTTTTGGGTACGGGGTCATGCTTCTCGAGCTCATCACTGGACAAAAGGCTTTTCGATCTT
35 GCTCGGCTTGCAAATGATGATGATATCATGTTACTCGACTGGGTGAAAGAGGTTTTGAAA
GAGAAGAAGTTGGAAGCCTTGTGGATGCAGAACTCGAAGGAAAGTACGTGGAACAGAA
GTGGAGCAGCTGATACAAATGGCTCTGCTCTGCACTCAAAGTTCTGCAATGGAACGTCCA
AAGATGTCAGAAGTAGTGAGAATGCTGGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAA
TGGCAAAAGGAGAGATGCCAATACATGATTTTAACATCAAGCCTATCCTCATGCTGGC
40 ACTGACTGGCTCATCCCTATTCCAATTCCTTATCGAAAACGATTACCCCTCGGGGCCA

AGATAAaccttttagaaagggtcatttcttgggttcttcaacaagtatatataggtgta
gtgaagttgtaagaagcaaaacccacattcacctttgaatatcactactctataa (SEQ ID NO: 60)

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS12 protein.

Different domains are spaced and shown from the N-terminus
10 towards the C-terminus. Overall domain structure is similar as
described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains a
leucine zipper motif, containing 2 leucine residues, each
15 separated by seven other amino acids. The third domain
contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain
20 contains many serine and proline residues, and is likely to
contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
domains are positioned. The seventh domain has an unknown
25 function. The eighth domain represents a serine / threonine
protein kinase domain (Schmidt et al. 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
domain at the C-terminal end represents part of a single
30 leucine rich repeat, probably involved in protein / protein
interactions.

MEHGSSRGFI

WLILFLDFVSRVTGKTQV

35

DALIALRSSLSSGDHTNNILQ

SWNATHVT

PCSWFHVTCNTENSVTRL

DLGSANLSGELV

P QLAQLPNLQYLELFNNTGEI

5 PEELGDLMEVLVSLOLFANNISGPI
PSSLGKLGKLRFLRLYNNLSGEI
PRSLTALP LDVLDISNNRLSGDI
PVNGSFSQFTSMRFA NNKLRR

10 PASPSPSPSGGTS

AAIVVGVAAGAALLFALAWWL

RRKLQGHFLDVPAAEEDPE

15 VYLGQFKRFSRLRELLVAT

EKFSKRNVLGKGRFGILYKGRAD

DTLVAVKRLNEERTKGGELQFQ

TEVEMISMAVHRNLLRLRGFCM

20 TPTERLLVYPYMANGSVASCLR

ERPEGNPALDWPKRKHIALGSA

RGLAYLHDHCDQKIIHLDVKAA

NILLDEEFVAVGDFGLAKLMN

YNDSHVTTAVRGTTIGHIAPEYL

25 STGKSSEKTDVFGYGVMLLELI

TGQKAFDLARLANDDDIMLLDW

VKEVLKEKKLESIVDAELEGKY

VETEVEQLIQMALLCTQSSAME

RPKMSEVVRMLE

30

GDGLAERWEEWQKEEMPIHDFNYQAY

PHAGTDWLIPYSNSLIENDYPSGPR (SEQ ID NO: 61)

35

Arabidopsis thaliana RKS13 cDNA

The start codons encoding predicted the methionine residue of the gene product has been indicated by bold capitals. The first stopcodon has been underlined.

- 5 Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

taataaacctctaataataatggctttgcttttactctgatgacaagttcaaaa**ATGGAA**
10 CAAAGATCACTCCTTTGCTTCCTTTATCTGCTCCTACTATTCAATTTCACTCTCAGAGTC
GCTGGAAACGCTGAAGGTGATGCTTTGACTCAGCTGAAAAACAGTTTGTATCAGGTGAC
CCTGCAAACAATGTACTCCAAAGCTGGGATGCTACTCTTGTTACTCCATGTACTTGGTTT
CATGTTACTTGCAATCCTGAGAATAAAGTTACTCGTGTGACCTTGGGAATGCAAACTA
TCTGGAAAGTTGGTTCCAGAACTTGGTCAGCTTTTAACTTGCAGTACTTGGAGCTTTAT
15 AGCAATAACATTACAGGGGAGATACCTGAGGAGCTTGGCGACTTGGTGAACTAGTAAGC
TTGGATCTTTACGCAAACAGCATAAGCGGTCCCATCCCTTCGTCTCTTGGCAAACCTAGGA
AAACTCCGGTCTTGGCTCTTAACAACAATAGCTTATCAGGGGAAATTCCAATGACTTGT
ACTTCTGTGTCAGCTGCAAGTTCTGGATATCTCAAACAATCGGCTCAGTGGAGATATTCCT
GTTAATGGTCTTTTTTCGCTCTTCACTCCTATCAGTTTGGCAATAATAGCTTAACGGAT
20 CTTCCCGAACCTCCGCTACTTCTACCTCTCCTACGCCACCACCACCTTCAGGGGGGCAA
ATGACTGCAGCAATAGCAGGGGAGTTGCTGCAGGTGCAGCACTTCTATTGCTGTTCCA
GCCATTGCGTTTGCTTGGTGGCTCAGAAGAAAACACAGGACCACCTTTTTTGATGTACCT
GCTGAAGAAGACCCAGAGGTTCAATTTAGGACAACCTCAAAGGTTTACCTTGCGTGAACGT
TTAGTTGCTACTGATAACTTTAGCAATAAAAATGTATTGGGTAGAGGTGGTTTGGTAAA
25 GTGTATAAAGGACGTTTAGCCGATGGCAATCTAGTGGCTGTCAAAGGCTAAAAGAAGAA
CGTACCAAGGGTGGGGAACCTGCAGTTTCAAACCGAAGTTGAGATGATCAGTATGGCCGTT
CATAGGAACCTTGCTTCGGCTTCGTGGCTTTTGCATGACTCCAACCTGAAAGATTACTTGTT
TATCCCTACATGGCTAATGGAAGTGTGCTTCTTGTTTAAAGAGCGTCCTGAAGGCAAT
CCAGCACTTGATTGGCCAAAAGAAAGCATATTGCTCTGGGATCAGCAAGGGGGCTTGCG
30 TATTTACATGATCATTGCGACCAAAAAATCATTCACCGGGATGTTAAAGCTGCTAATATA
TTGTTAGATGAAGAGTTTGAAGCTGTTGTTGGAGATTTTGGGCTCGCAAAATTAATGAAT
TATAATGACTCCCATGTGACAACTGCTGTACGCGGTACAATTGGCCATATAGCGCCCGAG
TACCTCTCGACAGGAAAATCTTCTGAGAAGACTGATGTTTTTGGGTACGGGTCATGCTT
CTCGAGCTCATCACTGGACAAAAGGCTTTCGATCTTGCTCGGCTTGCAAATGATGATGAT
35 ATCATGTTACTCGACTGGGTGAAAGAGGTTTTGAAAGAGAAGAAGTTGGAAAGCCTTGTG
GATGCAGAACTCGAAGGAAAGTACGTGGAACAGAAGTGGAGCAGCTGATACAAATGGCT
CTGCTCTGCACTCAAAGTTCTGCAATGGAACGTCCAAAGATGTCAGAAGTAGTGAGAATG
CTGGAAGGAGATGGTTTAGCTGAGAGATGGGAAGAATGGCAAAAGGAGAGATGCCAATA
CATGATTTTAACTATCAAGCCTATCCTCATGCTGGCACTGACTGGCTCATCCCCTATTCC
40 AATTCCTTATCGAAAACGATTACCCCTCGGGTCCAAGATAAAccttttagaaaggtctt

ttcttggtgggttcttcaacaagtatatatatagattggtgaagttttaagatgcaaaaaa
aa (SEQ ID NO: 62)

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS13 protein.

Different domains are spaced and shown from the N-terminus
towards the C-terminus. Overall domain structure is similar as
10 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains
leucine zipper motifs, containing 2 times 2 leucine residues,
each separated by seven other amino acids. The third domain
15 contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain
contains many serine and proline residues, and is likely to
20 contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
domains are positioned. The seventh domain has an unknown
function. The eighth domain represents a serine / threonine
25 protein kinase domain (Schmidt et al. 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
domain at the C-terminal end represents part of a single
leucine rich repeat, probably involved in protein / protein
30 interactions.

MEQRSLLCFLYLL
LLFNFTLRVAGNAEG

35 DALTQLKNSLSSGDP
ANNVLQSWDATLVT

PCTWFHVTCNPENKVTRV

DLGNAKLSGKLV
P ELGQLLNLYLELYSNNITGEI
PEELGDLVELVSLDLYANSISGPI
5 PSSLGKLGKLRFLRLNNSLSGEI
PMTLTSVQLQV LDISNNRLSGDI
PVNGSFSLFTPISFANNSLTDLPE

PPPTSTSPTPPPPSG
10 GQMTAAIAGGVAAGAAL
LFAVPAIAFAWWL

RRKPQDHFFDVPGAEDPE
15 VHLGQLKRFTLRELLVAT

DNFSNKNVLGRGGFGKVYKGRAD
GNLVAVKRLKEERTKGGELQFQ
TEVEMISMAVHRNLLLRGFCM
20 TPTERLLVYPYMANGSVASCLR
ERPEGNPALDWPKRKHIALGSA
RGLAYLHDHCDQKI IHRDVKAA
NILLDEEFEAVVGDFGLAKLMN
YNDSHVTTAVRG TIGHIAPEYL
25 STGKSSEKTDVFGYGVMLLELI
TGQKAFDLARLANDDDIMLLDW
VKEVLKEKKLESIVDAELEGKY
VETEVEQLIQMALLCTQSSAME
RPKMSEVVRMLE
30 GDGLAERWEEWQKEEMPIHDFNYQA

YPHAGTDWLIPYSNSLIENDYPSGPR (SEQ ID NO: 63)
35

Arabidopsis thaliana RKS14 cDNA

The start codon encoding the first predicted methionine residue of the gene product has been indicated by bold capitals.

5 The first stopcodon has been underlined.

Nucleotides predicted to encode protein sequences are in capitals. Leader and trailer sequences are in lowercase letters.

10 ctgcaccttagagattaataactctcaagaaaaacaagttttgattcggacaaag**ATG**TG
CAAGGAAGAAGAGAAGCAAAAAGAGTTATGCTTTGTTCTCTCAACTTTCTTCTTCTC
TTTATCTGTTTTCTTCTTCTTCTTCTGCGAAGTTCACAGACAAAGTTGTTGCCTTAATA
GGAATCAAAGCTCACTGACTGATCCTCATGGAGTTCTAATGAATTGGGATGACACAGCA
GTTGATCCATGTAGCTGGAACATGATCACTTGTCTGATGGTTTTGTCATAAGGCTAGAA
15 GCTCCAAGCCAAAACCTTATCAGGAACCTTTTCATCAAGTATTGGAAATTTAACAAATCTT
CAAACGTATACAGGTTATTGCGAACAATTACATAACAGGAAACATCCCTCATGAGATT
GGGAAATTGATGAAACTCAAACACTTGATCTCTCTACCAATAACTTCCTGGTCAAATC
CCATTCACTCTTTCTTACTCCAAAATCTTCACAGGAGGGTTAATAATAACAGCCTGACA
GGAACAATTCCTAGCTCATTTGGCAAACATGACCCAACTCACTTTTTGGATTTGTCGTAT
20 AATAACTTGAGTGGACCAGTTCCAAGATCACTTGCCAAAACATTCAATGTTATGGGCAAT
TCTCAGATTTGTCCAACAGGAACGAGAAAGACTGTAATGGGACTCAGCCTAAGCCAATG
TCAATCACCTTGAACAGTTCTCAAAGAACTAAAAACCGGAAAATCGCGGTAGTCTTCGGT
GTAAGCTTGACATGTGTTTGCTTGTGATCATTGGCTTTGGTTTTCTTCTTTGGTGGAGA
AGAAGACATAACAAACAAGTATTATTCTTTGACATTAATGAGCAAAACAAGGAAGAAATG
25 TGTCTAGGGAATCTAAGGAGGTTAATTTCAAAGAACTTCAATCCGCAACTAGTAACCTC
AGCAGCAAGAATCTGGTCCGAAAAGGAGGGTTTGAAATGTGTATAAAGGTTGTC'TTCAT
GATGGAAGTATCATCGCGGTGAAGAGATTAAAGGATATAAACAATGGTGGTGGAGAGGTT
CAGTTTCAGACAGAGCTTGAAATGATAAGCCTTGCCGTCCACCGGAATCTCCTCCGCTTA
TACGGTTTCTGTACTACTTCTCTGAACGGCTTCTCGTTTATCCTTACATGTCCAATGGC
30 AGTGTGCTTCTCGTCTCAAAGCTAAACCGGTATTGGATTGGGGCACAAAGAAAGCGAATA
GCATTAGGAGCAGGAAGAGGGTTGCTGTATTGTCATGAGCAATGTGATCCAAAGATCATT
CACCGTGATGTCAAAGCTGCGAACATACTTCTTGACGATTACTTTGAAGCTGTTGTGCGGA
GATTCGGGTTGGCTAAGCTTTTGGATCATGAGGAGTCGCATGTGACAACCGCCGTGAGA
GGAACAGTGGGTCACATTGCACCTGAGTATCTCTCAACAGGACAATCTTCTGAGAAGACA
35 GATGTGTTGCGTTTCGGGATTCTTCTCTCGAATTGATTACTGGATTGAGAGCTCTTGAA
TTCGAAAAGCAGCAAAACCAAGAGGAGCGATACTTGATTGGGTAAAGAACTACAACAA
GAGAAGAAGCTAGAACAGATAGTAGACAAGGATTTGAAGAGCAACTACGATAGAATAGAA
GTGGAAGAAATGGTTCAAGTGGCTTTGCTTTGTACACAGTATCTTCCCATTCACCGTCCT
AAGATGTCTGAAGTTGTGAGAATGCTTGAAGGCGATGGTCTTGTTGAGAAATGGGAAGCT
40 TCTTCTCAGAGAGCAGAAACCAATAGAAGTTACAGTAAACCTAACGAGTTTTCTTCCTCT

GAACGTTATTTCGGATCTTACAGATGATTCCTCGGTGCTGGTTCAAGCCATGGAGTTATCA
GGTCCAAGATGAcaagagaaactatatgaatggctttgggtttgtaaaaaa (SEQ ID NO: 64)

5

Predicted amino acid sequence of the *Arabidopsis thaliana*
RKS14 protein.

Different domains are spaced and shown from the N-terminus
towards the C-terminus. Overall domain structure is similar as
10 described in Schmidt et al. (1997).

At the predicted extracellular domain the first domain
represents a signal sequence. The second domain contains a
leucine zipper motif, containing 3 leucine residues, each
separated by seven other amino acids. The third domain
15 contains conserved cysteine residues, involved in disulphate
bridge formation. The fourth domain contains a leucine rich
repeat domain, consisting of 5 complete repeats of each
approximately 24 amino acid residues. The fifth domain
contains many serine and proline residues, and is likely to
20 contain hydroxy-proline residues, and to be a site for O-
glycosylation. The sixth domain contains a single
transmembrane domain after which the predicted intracellular
domains are positioned. The seventh domain has an unknown
function. The eight domain represents a serine / threonine
25 protein kinase domain (Schmidt et al. 1997) and is probably
also containing sequences for protein / protein interactions.
The ninth domain has an unknown function. The last and tenth
domain at the C-terminal end represents part of a single
leucine rich repeat, probably involved in protein / protein
30 interactions.

MLQGRREAKKSYALFSSTFF
FFFICFLSSSSAELTDKV

35

VALIGIKSSLTDP
HGVLNWDDTAVD

PCSWNMITCSDGFVIR

LEAPSQNLSGTLSS
SIGNLTNLQTVYRLLQNNYITGNI
PHEIGKLMKLKTLDLSTNNFTGQI
5 PFTLSYSKNLHRRV NNNSLTGTI
PSSLANMTQLTFDLSYNNLSGPV
PRSLAKTFNVMGNSQICPT

GTEKDCNGTQPKMSITLNSSQR
10 TKNRK

IAVVEGVSLTCVCLLIIGFGFLLWW

RRRHNKQVLFFDINEQNKE
15 EMCLGNLRRFNFKELQSAT

SNFSSKNLVGKGGFGNVYKGCLHD
GSIIAVKRLKDINNGGGEVQFQ
TELEMISLAVHRNLLRLYGECT
20 TSSERLLVYPYMSNGSVA
SRLKAKPVLDWGTRKRIALGAG
RGLLYLHEQCDPKIIHRDVKAA
NILLDDYFEAVVGDFGLAKLLD
HEESHVTTAVRGTVGHIAPEYL
25 STGQSSEKTDVFGFGILLLELI
TGLRALEFGKAANQRGAILDW
VKKLQQEKKLEQIVDKDLKSNY
DRIEVEEMVQVALLCTQYLPFH
RPMSEVVRMLE
30
GDGLVEKWEASSQRAET
NRSYSKPNEFSSS

ERYSDLTDDSSVLVQAMELSGPR (SEQ ID NO: 65)
35

Legends

Figure 1

5

The different domains of the predicted RKS gene product have the following functions:

The first domain of the predicted protein structure at the N-terminal end consists of a signal sequence, involved in
10 targeting the protein towards the plasma membrane. Protein cleavage removes this sequence from the final mature protein product (Jain et al. 1994, J. Biol. Chemistry 269: 16306-16310). The second domain consists of different numbers of leucine zipper motifs, and is likely to be involved in protein
15 protein dimerization. The next domain contains a conserved pair of cystein residues, involved in disulphate bridge formation. The next domain consists of 5 (or in the case of RKS3 only 4) leucine rich repeats (LRRs) shown in a gray colour, likely to be involved in ligand binding (Kobe and
20 Deisenhofer 1994, TIBS 19: 415-420). This domain is again bordered by a domain containing a conserved pair of cystein residues involved in disulphate bridge formation often followed by a serine /. proline rich region. The next domain displays all the characteristics of a single transmembrane
25 domain (<http://genome.cbs.dtu.dk/services/TMHMM/>). At the predicted cytoplasmic site of protein a domain is situated with unknown function, followed by a domain with serine /threonine kinase activity (Schmidt et al. 1997, Development 124: 2049-2062). The kinase domain is followed by a domain
30 with unknown function whereas at the C-terminal end of the protein part of a leucine rich repeat is positioned, probably involved in protein-protein interactions.

Figure 2

35

Alagntment of the predicted protein sequences of the different RKS gene products from *Arabidopsis thaliana* with alignX, Vector NTI Suite 5.5 resulted in a phylogenetic tree in which

the relative homology between the different RKS members is shown.

Figure 3

- 5 Intron-Exon boundaries of the genomic regions on the chromosomes of *Arabidopsis thaliana* encoding the different RKS gene products. Exons are shown as boxes, whereas intron sequences are shown as lines. Sequences encoding LRR domains are displayed in gray colour, transmembrane regions in black.

10

Figure 4.

Cromosomal location of RKS genes in *Arabidopsis thaliana*, showing colocalisation with GASA genes.

- 15 Figure 5. A signaling complex comprising molecules of RKS proteins, ELS proteins, NDR/NHL proteins and SBP/SPL proteins.

Figure 6.

- 20 Second generation (T2) tobacco seedlings germinated on MS medium. Transformations were performed with DNA clone 2212-15, representing the overexpression construct GT-RKS4-s. T2 seedlings derived from T1 plant 15.7 shows co-suppression effects while T1 plant 15.6 shows no obvious changes in level of RKS4. T1 plants 15.9 and 15.3 show overexpression effects.
- 25 Plant 15.7 has the lowest remaining level of RKS4 gene product, whereas plant 15.3 has the highest level of RKS4 gene product.

Figure 7

- 30 Second generation (T2) tobacco plants. In the upper row the offspring from a co-suppressing T1 plant 15.7 is shown. The middle row shows plants derived from a transgenic T1 plant 15.6 with no clear changes in level of RKS4 is shown while the bottom row shows plants derived from a T1 plant 15.3 in which
- 35 the levels of RKS4 are increased by the introduction of the overexpression construct GT-RKS4-s.

Figure 8

Second generation (T2) tobacco plants. Plants derived from a co-suppressing T1 plant 15.7 show a reduction in plant size and a delay in the initiation and outgrowth of primordia. The control empty vector transgenic plants show no visible differences in growth compared with the offspring from the transgenic 15.6 plant, in which the endogenous level of RKS4 gene product was not changed. In the overexpressing plants 15.9 and 15.3 organ size was increased, similar as the number of initiated leaf primordia.

Figure 9

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is decreased (right picture) due to the presence of a transgenic RKS4 antisense construct (GT-RKS4-16a). The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia is decreased in the transgenic antisense plant compared with the wildtype control.

Figure 10

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is decreased (bottom left picture) due to the presence of a transgenic RKS4 antisense construct (GT-RKS4-16a). The upper right picture shows a wildtype flower of the same age as the transgenic antisense flower, grown under similar growth conditions. Total flower size is only slightly decreased in the transgenic antisense flower compared with the control flower, whereas organ size of petals is strongly decreased.

Arabidopsis thaliana WS plants in which the endogenous level of RKS4 gene product is increased (upper left picture) due to the presence of a transgenic RKS4 overexpressing construct (GT-RKS4-6s). Compared with the wildtype control flower, total flower size of the transgenic flower is clearly increased. Both sepal and petal organ size is clearly increased compared

with the control.

For comparison an *Arabidopsis thaliana* WS plant is shown which has been transformed with a construct encoding the GAS3 gene in sense direction, i.e. overexpressing GAS3.

5

Figure 11.

Formation of meristematic regions in the hypocotyl of *Arabidopsis thaliana* WS plants under influence of overexpression of RKS4.

- 10 RKS4 overexpression results in increases in flower and seed organ size that could be due to increase in cell elongation and/or cell division. In order to analyse the cell division patterns in plants with deregulated RKS4 expression the mitotic activity in transgenic plants was analyzed with the a
- 15 unstable GUS reporter under the control of a cyclin B1;1 promoter (the Plant Journal 1999 (4) 503-508 Spatio-temporal analysis of mitotic activity with a labile cyclin-GUS fusion protein). *Arabidopsis thaliana* WS seedlings with the pCDG construct did not show gus activity (cell division) in
- 20 hypocotyls (top) whereas the same pCDG line crossed with a constitutive RKS4 construct showed mitotic activity as indicated by GUS-positive cells (bottom); indicating that RKS4 overexpression activated mitotic activity in hypocotyls.

25

Figure 12

In *Arabidopsis thaliana* WS, the seed size is influenced by changing levels of RKS4 gene product. Constitutive overexpression of RKS4 results in increases in seed size (left) compared with control wildtype seeds (right). Antisense

30 constitutive expression of RKS4 cDNA (middle) results in a decrease in seed size compared with the control (right). Magnification is identical in all photos as shown by the bar size.

35

Figure 13

Organ size can be influenced by either modulating cell division or cell elongation or a combination of both. In order to identify the total number of cells and the cell size within an organ the apical site of petals of mature *Arabidopsis* flowers was investigated. Petal organ size is clearly influenced by modulation of RKS4 gene product levels (bottom row for the flowers from which the apical petal epidermal cells were identified). Epidermal cell size is not changed in transgenic plants compared with the control.

10

Figure 14

Arabidopsis thaliana WS plants in which the endogenous level of RKS10 gene product is increased (right picture) due to the presence of a transgenic RKS10 overexpressing construct. The left picture shows the apical epidermus of a full grown cotyl from an empty vector transgenic seedling of the same age as the transgenic overexpressing cotyl, grown under similar growth conditions..

20 Figure 15

Arabidopsis thaliana WS plants in which the endogenous level of RKS10 gene product is decreased (right picture) due to the presence of a RKS10 antisense construct The left picture shows a wildtype plant of the same age as the transgenic antisense plant, grown under similar growth conditions. Plant size, organ size and number of organ primordia remains similar in both the transgenic antisense plants and the wildtype control.

30 Figure 16

In order to determine organ size variations in transgenic RKS10 transgenic plants compared with empty vector control transgenic plants (pGreen4K), flower organ size was determined of the four open flower stages of *Arabidopsis* inflorescences. The four successive flower stages are photographed under similar magnifications. No obvious changes in organ length could be observed in size of sepals, petals, stamen and carpel

between empty vector control flowers (pGreen4K), flowers with an antisense RKS10 construct (a) or plants overexpressing the RKS10 cDNA under the control of a 35S promoter (S

5 Figure 17

Tissue cultured auxin treated *transgenic Arabidopsis* T2 seedlings were grown on MS agar plates without hormones for a period of 3 weeks. Regeneration potential was scored and the formation and outgrowth of multiple shoot apical meristems from single seedling origin was displayed as (+). The formation and outgrowth of only one shoot apical meristem, leading to the formation of a normal rosette of leaves from individual plants was displayed as (-). Positive regeneration controls consisted of seedlings overexpressing either KNAT1, CUC2, IPT or cycD3. All of these showed an increase of regeneration capacity (+) compared with a negative control GUS overexpressing plant pGreen5K (-). Representative examples of RKS and ELS cDNA overexpressing (s) or antisense (a) cosuppressing constructs in *transgenic* plants are shown in the bottom panels.

Figure 18.

Tobacco leaf discs were stably transformed with the RKS0 overexpressing construct GT-RKS0-23S and from a single transformation event, large numbers of regeneration plantlets were isolated and subcultured. All of the regenerated plants were potted and flowered. The original transformation event could be kept continuously in tissue culture indefinitely.

30 Figure 19

Seedlings from *transgenic Arabidopsis thaliana* containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in which fasciation could be routinely observed are shown together with a negative control plant (pGreen5K, overexpressing the GUS gene) in which fasciation could never be observed.

Figure 20 - 23

Primary root tips of transgenic *Arabidopsis* plants (top rows) photographed under similar magnification. The bottom rows show the corresponding seedlings (also between each other under the same magnification). Figure 23 shows the specific *Arabidopsis* transgenes with a strong increase in root outgrowth.

Figure 24

Average root length of 10-30 transgenic *Arabidopsis* T2 seedlings from one T1 transgenic plant is shown.

Figure 25

T3 seedlings are shown from a strong co-suppressing RKS10 antisense construct line (T1-4; T2-6; T3 generation) and a strong overexpressing line (T1-4; T2-6; T3 generation). The overexpressing line is different and stronger from the one shown in Figure 4.1-4.5. Pictures are taken under similar magnifications.

Figure 26

T2 seed was germinated on horizontal MS agar plates and pictures were taken under similar magnification of representative examples of the lateral root development from transgenic RKS and ELS transgenic roots.

Figure 27

Pictures taken from transgenic RKS8 or RKS10 overexpressing roots taken directly behind the tip zone. Pictures are taken under same magnification.

Figure 28

Arabidopsis thaliana WS plants in which the endogenous level of RKS or ELS gene product is modified result in the formation of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants compared with control empty vector control plants (pGreen4K).

Overexpression of RKS10 and ELS1 (S) and cosuppression with antisense constructs of RKS8 and also RKS10, result in increased numbers of developing generative meristems. The generative shoots are photographed with similar magnification.

Figure 29

Arabidopsis thaliana WS plants in which the endogenous level of RKS gene product is modified result in the formation of new meristem formation and / or outgrowth, resulting in a complex, bushy inflorescence in transgenic *Arabidopsis* plants compared with control empty vector control plants (pGreen4K). The top panel shows adult plants under similar magnification. Compared with the control, RKS10 overexpression results in an extreme bushy phenotypic plant. The results of co-suppressing the RKS8 gene product are less dramatic with respect to the bushiness. However, also in these transgenic plants the number of generative meristems is strongly increased compared with the control. The bottom panel shows the generative shoot in detail under similar magnification.

Figure 30

Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in transgenic *Arabidopsis* plants containing an antisense (a) RKS10 construct. The terminal flower meristem produces 2 sepals, 1 petal, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. Two new flowers are protruding from this structure, containing all flower organs in normal numbers.

Figure 31

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in transgenic *Arabidopsis* plants T1-11 containing an antisense (a) RKS10 construct. The

terminal flower meristem produces 1 sepal, 2 petals, 2 stamen, a carpel which is not a closed structure but open with groups of ovules on the inside and outside of this structure, and stigmatic cells protruding from the top part. An undetermined
5 flower meristem is protruding from the open carpel structure and forms a number of new flowers, including normal flowers (right) and another abnormal flower (left) which consists of a flower with half of the sepal, petal and stamen organs formed and a new terminal flower meristem protruding from this
10 structure, developing in structures as seen in Figure 7.5. The stamen contain only small numbers of (viable) pollen compared with wildtype stamen (see also chapter 5).

Figure 32

15 Schematic drawing of the different flower organs in an empty vector control pGreen4K flower (left) compared with a complex transgenic flower structure seen in a transgenic *Arabidopsis* plant T1-11 containing an antisense (a) RKS10 construct (overview shown in Figure 7.4). The terminal flower meristem
20 produces half the normal number of sepals, petals and stamen. The remaining part of the flower structure has converted into a new structure containing a new stem containing a single organ structure resembling a fusion between a petal and a sepal. On this structure several (viable) pollen grains can be
25 observed.

Figure 33

Schematic drawing of the different flower organs in a complex transgenic flower structure seen in a transgenic *Arabidopsis*
30 plant T1-12 containing an antisense (a) RKS10 construct. The terminal flower meristem originating from an undetermined generative meristem is here producing an axillary secondary undetermined meristem (left picture), a single organ resembling a stamen (bottom left), a normal flower and a
35 terminal flower. This terminal flower structure contains 2 normal sepals, 2 normal petals, 2 normal stamen (with only a few viable pollen) and two organs resembling a fusion of

sepals /petals/stamen (see also figure 7.7). From this terminal flower structure two new flowers emerge (in a similar fashion as observed in Figure 7.3) containing normal numbers of flower organs (right photos). At the top of this figure a control inflorescence is shown schematically with terminal flower meristems as normally originate from the generative *Arabidopsis thaliana* generative meristem.

Figure 34

Schematic drawing and detailed pictures of several of the structures as shown in figure 7.6. At the right the organs resembling a fusion between sepals/petals/stamen are shown with viable pollen sticking out from these structures. At the top left the single stamen-like organ directly protruding from the main stem is shown.

Figure 35

Transgenic *Arabidopsis* plants overexpressing the RKS13 gene product show a modification of the normal flower inflorescence architecture, somewhat resembling the structures observed in RKS10 antisense plants. A terminal flower containing a normal seed developing silique and a small number of sepals, petals and stamen, develops at least 4 additional terminal flower meristems that develop abnormally themselves, resulting in open carpel structures and modifications of organ structures.

Figure 36

Transgenic plants in which the RKS and / or ELS genes are introduced behind a constitutive 35S promoter in an overexpressing (S) or antisense (a) configuration are analyzed for sterility and characterized further for defects in proper pollen development. As a negative control the normal pollen development of a transgene containing the empty expression vector (pG4K) was included. First generation transgenic flowers of RKS10 expressing constructs and second generation control vector and ELS2 are shown under similar magnification. In detail the stigmatic surface and surrounding stamen, are

shown under similar magnification, showing the presence or absence of pollen on the stamen or the stigmatic surface.

Detailed description

1.Modifying organ size

5

Plant size is determined by both cell elongation and cell division rate. Modifying either one or both processes results in a change in final organ size. Increasing the level of specific members of the family of RKS genes results in an increase in organ size, growth rate and yield. Modulating plant growth, organ size and yield of plant organs is the most important process to be optimized in plant performance. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent thereof. Inactivation of endogenous RKS gene product results in a decrease in plant growth, proving that the normal function of these endogenous RKS gene products is the regulation of growth and organ size. Elevation of the levels of the regulating of the RKS signaling complex in plant cells is provided in order to increase:

- the size of plant organs
- the growth rate
- the yield of harvested crop
- the yield of total plant material
- the total plant size

Decreasing the levels of endogenous RKS gene product is provided in order to decrease:

- the size of plant organs

the growth rate
the total plant size

5

Results obtained (see also figures 6 to 13)

Overexpression and antisense constructs of full length RKS
cDNA clones have been made under the control of 35S
promoters. Transgenic plants have been produced in *Arabidopsis*
10 *thaliana* and in *Nicotiana tabacum*. Subsequent generations of
stably transformed plants were investigated for phenotypes and
analyzed in detail. The phenotype observed in transgenic
plants with antisense constructs of RKS4 (GT-RKS4-a) could be
described as dwarf plants in which all plant organs showed a
15 decrease in organs size and growth rate. Overexpression of
RKS4 (GT-RKS4-s) resulted in plants with increased size of
organs and an increase in growth rate. Since cell size alone
was not responsible for the modifications in organ size of
petals it can be concluded that RKS4 is involved in the
20 regulation of the cellular divisions during plant growth and
organ formation. Overexpression of RKS 4 results in an
increase of cellular divisions whereas a decrease in
endogenous RKS 4 gene product levels within the plant results
in a decrease of cellular division rates.

25

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2. Cell division

The mitotic cell cycle in eukaryotes determines the total number of cells within the organism and the number of cells within individual organs. The links between cell proliferation, cell differentiation and cell-cycle machinery are of primary importance for eukaryotes, and regulation of these processes allows modifications during every single stage of development. Here we show that modulating the level of members of the family of the RKS signaling complex is sufficient to modulate these processes. The invention provides herewith a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating cellular division during plant growth or organ formation, in particular wherein said gene comprises an RKS4 or RKJS 10 gene or functional equivalent. Herewith the invention provides a method for modulating the number of cells to be formed within an eukaryotic organism as a whole or for modulating the cell number within individual organs is, which of primary importance in modulating plant developmental processes, especially of arable plants. Here we show that members of the RKS signaling complex are able to regulate the number of cellular divisions, thereby regulating the total number of cells within the organism or different organs.

30 Possible Applications

Elevation of the levels of the regulating RKS signaling complex members in plant cells in order to increase:
the size of plant organs
the growth rate
35 the yield of harvested crop
the yield of total plant material
the total plant size

- Decreasing the levels of endogenous RKS signaling complex members in order to decrease:
the size of plant organs
5 the growth rate
the total plant size

Results obtained

- Overexpression and antisense constructs of full length RKS
10 cDNA clones have been made under the control of 35S
promoters. Transgenic plants have been produced in *Arabidopsis thaliana* and in *Nicotiana tabacum*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.
- 15 Overexpression of RKS 4 results in an increase of cellular divisions whereas a decrease in endogenous RKS 4 gene product levels within the plant results in a decrease of cellular division. Another example of RKS genes involved in cellular proliferation is provided by RKS10. Overexpression of RKS10
20 (S) results in a decrease in apical epidermal cells (Figure 14) compared with control plants containing an empty expression cassette (pGreen4K). Co-suppressing the endogenous RKS 10 gene in plants containing an antisense construct (a) showed clearly larger epidermal cells as the corresponding
25 cells in wildtype control plants (Figure 15). In contrast to the plant phenotypes shown in RKS4 transgenic plants, no differences in plant or organ size could be observed in the RKS10 transgenic plants or organs. This shows that although the organ size remains constant, the number of cells within
30 these organs is variable due to the differences in size of individual cells. These results indicate that normal RKS4 function within the plant can be described as an activator of cellular division.
- Normal RKS10 function also involves an activation process on
35 cellular division rate. This effect is also detectable in the root in the region directly behind the tip zone, where in the RKS10 overexpressing transgenes cellular divisions were

detectable in a region where normally cell proliferation has ceased. The plane of divisions of root cells in these transgenes is also clearly different from the normal plane of root cell division, resulting in clumps of cells with all

5 types of division planes possible.

In contrast to RKS4, the final organ size in RKS10 transgenic plants is under the control of other organ size restriction processes, in such a way that the final organ volume remains constant (Figure 16). RKS4 and RKS10 are essentially involved

10 in the same cell cycle activation process, but either addition organ size controlling functions of these RKS genes or the hierarchical order in which they regulate the cell cycle is different.

15

Literature

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3. Regeneration

Modification the levels of different RKS and ELS genes within
5 plants allows the initiation and / or outgrowth of apical
meristems, resulting in the formation of large numbers of
plantlets from a single source. A number of gene products that
is able to increase the regeneration potential of plants is
known already. Examples of these are KNAT1, cycD3, CUC2 and
10 IPT. Here we show that modulation of the endogenous levels of
RKS genes results in the formation of new shoots and plantlets
in different plant species like *Nicotiana tabacum* and
Arabidopsis thaliana. herewith the invention provides a method
for modulating a developmental pathway of a plant or plant
15 cell comprising modifying a gene or modifying expression of
said gene, wherein said gene is encoding a protein belonging
to a signaling complex comprising RKS protein, ELS protein,
NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein,
allowing modulating apical meristem formation, in particular
20 wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or
RKS10 gene or functional equivalent thereof. A direct
application of a method according to the invention is the
stable or transient expression of RKS and ELS genes or gene
products in order to initiate vegetative reproduction.
25 Regeneration can be induced after overexpression of for
example RKS0 and ELS1; or by co-suppression of for example the
endogenous RKS3, RKS4, RKS8 or RKS10 genes. Overexpression or
co-suppression of these RKS and ELS gene products can be
either transient, or stable by integration of the
30 corresponding expression cassettes in the plant genome.

Results obtained

Overexpression and antisense constructs of full length RKS and
ELS cDNA clones have been made under the control of 35S
35 promoters. Transgenic plants have been produced in *Arabidopsis*
thaliana and in *Nicotiana tabacum*. Subsequent generations of

stably transformed plants were investigated for phenotypes and analyzed in detail.

T2 transgenic seedlings of *Arabidopsis* were germinated in liquid MS medium supplemented with 1 mg/L 2,4-D for 1 week,
5 followed by extensive washing and plating of the seedlings onto MS agar plates without hormones. Control transgenic seedstocks containing either a negative control vector (pGreen5K); or positive control overexpression constructs of gene products known to increase the regeneration potential
10 (IPT, KNAT1, CUC2 and cycD3) were characterized for regeneration potential together with seedstocks from plants either overexpressing (s) or co-suppressing (a) all RKS and ELS gene products (Figure 17). Overexpression of the ELS1 and RKS0 cDNA clones resulted in an increase of shoot apical
15 meristem formation and outgrowth, whereas antisense constructs (a) of these cDNA clones did not increase the regeneration potential (only increased regeneration results are shown). Antisense constructs of RKS3, RKS4, RKS8 and RKS10 also resulted in an increased formation and outgrowth of apical
20 meristems (Figure 17).

T1 generation *Nicotiana tabacum* tissue cultures transformed with ELS and RKS gene products in either overexpression (s) cassettes or antisense co-suppression (a) cassettes allowed the regeneration of indefinite number of offspring plants from
25 a single transformed cell origin (Figure 18). An example is shown for the overexpression of the GT-RKS0-23S construct. The resulting plants obtained from one transformation event in general showed no phenotypes. Only a subset of plants displayed RKS0 overexpression phenotypes (like loss of apical
30 dominance and early flowering).

Literature

-Mechanisms that control knox gene expression in the
35 *Arabidopsis* shoot. N. Ori et al. 2000, Development 127: 5523-5532

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4. Fasciation

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs.

Modulation of the number of cells within the proliferating zone of the shoot apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to stems in which the number of cells is increased. The invention herewith provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating fasciation, in particular wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof. Here we for example show that modulation of the levels of RKS gene products in plants like *Arabidopsis thaliana* can result in fasciated stems as shown in Figure 19. A direct application as provided herein is the regulated formation of fasciation in plant species in which such a trait is desired like ornamental plants. Regulation of the initiation and extent of fasciation, either by placing the responsible RKS encoding DNA sequences under the control of stage or tissue specific promoters, constitutive promoters or inducible promoters results in plants with localized or constitutive fasciation of stem tissue. Another application is modulating the number of primordia by regulation of the process of fasciation. An example is provided by for example sprouts, in which an increased number of primordia will result in an increased numbers of sprouts to be harvested. Fasciation can also result in a strong modification in the structural architecture of the inflorescence, resulting in a terminal group of flowers resembling the *Umbelliferae* type (an example is shown in Figure 19 where the fasciated meristem of a RKS0-7S *Arabidopsis* plant in which endogenous RKS0 gene product

levels have been deregulated clearly terminates in an *Umbelliferae* type inflorescence.

Results obtained

- 5 Overexpression and antisense constructs of full length RKS
cDNA clones have been made under the control of 35S
promoters. Transgenic plants have been produced in *Arabidopsis*
thaliana. Subsequent generations of stably transformed plants
were investigated for phenotypes and analyzed in detail.
- 10 T2 transgenic seedlings of *Arabidopsis* were germinated on MS
agar plates without hormones. Control transgenic seedstocks
containing a negative control vector (pGreen5K) were tested
for their ability to induce fasciation (Overexpression
constructs (s) of RKS0, RKS8 and RKS10 cDNA clones resulted in
15 fasciated plants, whereas antisense constructs (a) of these
cDNA clones did not increase the regeneration potential (only
positive results are shown). Antisense constructs of RKS3
gave also rise to fasciation (Figure 19).

20

Literature

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25 loop regulated by CLV3 activity.
U. Brand et al. 2000. Science 289: 617-619

5. Root development

Fasciation is normally a result from an increased size of the apical meristem in apical plant organs. Modulation of the number of cells within the proliferating zone of the root apical meristem results in an excess number of cellular divisions, giving rise to excess numbers of primordia formed or to roots in which the number of cells is increased. Adaptation to soil conditions is possible by regulation of root development of plants. Here we describe several processes in root development that can be manipulated by modification of the levels of the RKS signaling complex within the root. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein allowing modulating root development, in particular wherein said gene comprises an ELS1, ELS2, RKS1, RKS3, RKS4, RKS6 RKS8 or RKS10 gene or functional equivalent thereof. Root length, a result by either root cells proliferation or elongation, can for example be increased by overexpression of for example RKS3, RKS4, RKS6 and ELS2, or inactivation of the endogenous RKS10 gene product. Root length can also be decreased by decreasing of endogenous RKS1 levels or by strong overexpression of RKS10. The initiation of lateral roots is also regulated by RKS gene products. Overexpression of for example RKS10 can result in a strong increase in the initiation and outgrowth of lateral roots. Co-suppression of RKS1 also resulted in the initiation and outgrowth of large numbers of lateral roots. Root hair formation and elongation is important in determining the total contact surface between plant and soil. A strong increase of root hair length (elongation) can be obtained by overexpression of ELS1 and RKS3 gene products. As the roots of terrestrial plants are involved in the acquisition of water and nutrients, anchorage of the plant, synthesis of plant

hormones, interaction with the rhizosphere and storage functions, increasing or decreasing root length, for example for flexible adaptations to different water levels, can be manipulated by overexpressing or cosuppressing RKS and / or
5 ELS gene products. Modulation of the total contact surface between plant cells and the outside environment can be manipulated by regulation lateral root formation (increased by RKS10 overexpression and co-suppression of RKS1). Finally the
10 contact surface between plant cells and the soil can be influenced by modulation of the number of root hairs formed or the elongation of the root hairs, as mediated by ELS1 and RKS3.

Results obtained

15 Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail.
20 T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic seedstocks containing a negative control vector pGreen4K (empty expression vector) and / or pGreen5K (a GUS overproducing vector) were included as references for normal root
25 development. Seedlings from transgenic *Arabidopsis thaliana* containing either constructs overexpressing (s) or co-suppressing by antisense (a) the RKS gene products were screened for the appearance of fasciation. Several examples in
30 which fasciation could be routinely observed are shown together with a negative control plant (pGreen4K, containing an expressing cassette without an insert cDNA). Seedlings are germinated and grown on vertically placed MS agar plates.

35

Literature

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6. Apical meristems

All parts of the plant above the ground are generally the result on one apical shoot meristem that has been initiated
5 early at embryogenesis and that gives rise to all apical organs. This development of a single meristem into complex tissue and repeated patterns is the result of tissue and stage-dependent differentiation processes within the meristems and its resulting offspring cells. The control of meristem
10 formation, meristem identity and meristem differentiation is therefore an important tool in regulating plant architecture and development. Here we present evidence the function of RKS and ELS gene products in regulation of the meristem identity and the formation and outgrowth of new apical meristems. The
15 invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and
20 RKS/ELS ligand protein allowing modulating meristem identity, in particular wherein said gene comprises an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof. Introduction of for example the RKS10 gene product or an other member of the RKS signaling complex under the control of a tissue and /
25 or stage specific promoter as provided herein allows localized and time regulated increases in the levels of gene product. For example the meristematic identity in a determined meristem might thereby be switched back into an undetermined meristem, thereby changing for example a terminal flower into an
30 undetermined generative meristem.

Another application might be found in changing the meristematic identity at an early time point, during early vegetative growth, thereby switching the vegetative meristem into a generative meristem, allowing early flowering.

35 Modulation of meristem identity in terminal primordia, like for example as shown in Figure 30, where flower organ primordia are converted into terminal flower primordia, allows

the formation of completely new types of flowers and fused fruit structures. Constitutive overexpression of RKS gene products results in plants with many apical meristems, as can clearly been seen in Figure 29, where RKS10 overexpression
5 results in an extremely bushy phenotype.

Results obtained

Changing the normal levels of endogenous RKS10 within the
10 plant, either by overexpressing or co-suppressing the RKS10 cDNA, results in an increase in generative meristem development (Figure 28).

Compared with the control empty vector transgenic pGreen4K plants, large number of meristems are initiated at places were
15 normally no meristems initiate and / or develop. A clear example is shown by co-suppressing the RKS8 gene (Figure 29), where many new inflorescence meristems are initiated from the central generative meristem compared with control pGreen4K plants of the same age. This phenotype is even more extreme in
20 RKS10 overexpressing plants where the resulting plants are extremely bushy with very large numbers of generative meristems formed. Inactivation of the endogenous RKS10 gene in *Arabidopsis* results in modification of meristematic identity as can be shown in Figure 30. A determined flower meristem
25 develops into two new normal terminal flower meristems and a number of terminal flower organ primordia. Another example is shown in Figure 31 where meristem determination is switched from a terminal flower meristem, that normally result only in the normal numbers of terminal organ primordia, towards a
30 number of organ primordia, a new undetermined generative meristem that develop into normal flowers or in a new terminal flower meristem with developmental abnormalities. Only half of the terminal flower primordia develop normally while an extra structure arises resembling a new flower stem with a
35 petal/stamen like organ. The few pollen detectable on this structure (Figure 32) were able to pollinate a MS1 (male sterile) *Arabidopsis* flower. Figure 33 shows the meristematic

developmental switch from a terminal flower meristem into a new undetermined generative meristem, that gives rise to a new formation of another undetermined meristem, and several normal and abnormal terminal flowers. The abnormal flowers again show the fusion of different structures, in this case from sepals, petals and stamen together (Figure 34). Surprisingly, directly on the generative stem another structure, resembling a single stamen was detectable. All these data indicate that a decrease in RKS1 expression levels results in switches in the meristematic identity. Meristems can switch forward and backward between developmental stages, indicating that RKS10 is normally involved in regulating the meristematic identity and the developmental order of meristematic development. RKS13 seems to be involved in similar processes, as can be concluded from the switches in flower meristematic outgrowths observed in figure 35. Modification of the expression levels of RKS1 also results in modified meristem identity. Suppression of endogenous RKS1 levels results in a developmental switching of generative meristems towards vegetative meristems, together with other phenotypes (results not shown).

Literature

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- A genetic framework for floral patterning. F. Parcy et al. 1998 Nature 395: 561-566
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7. Male sterility

Male sterility is a highly desired trait in many plant species. For example, manipulation of pollen development is crucial for F1 hybrid seed production, to reduce labour costs and for the production of low-environmental impact genetically engineered crops. In order to produce hybrid seed from inbred plant lines, the male organs are removed from each flower, and pollen from another parent is applied manually to produce the hybrid seed. This labour-intensive method is used with a number of vegetables (e.g. hybrid tomatoes) and with many ornamental plants. Transgenic approaches, in which one or more introduced gene products interfere with normal pollen initiation and development is therefore highly desired. Especially when the number of revertants (growing normal pollen) is extremely low.

Male sterility in plants is a desired trait that has been shown already in many plant species as a result of the inactivation of expression of a number of genes essential for proper stamen development, mitotic divisions in the pollen stem cells, or male gametogenesis. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein, allowing modulating pollen development, in particular wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

Here we present data that show that overexpression of gene products, like transmembrane receptor kinases (RKS) and extracellular proteins (ELS) can also result in the formation of male sterility. The ability to induce male sterility by overexpressing specific genes as provided herein allows the opportunity to produce transgenic overexpressing plants in which the pollen development is inhibited. Stable single copy homozygous integration of such overexpressing traits into the

plant genome will render such plants completely sterile, making them excellent material for the production of F1 hybrid seed. Furthermore, the combined integration of a male sterility inducing overexpressing gene coupled directly with another desired transgene result in transgenic plants which are unable to produce transgenic seed, making these transgenic plants excellent material for outside growth without problems affecting transgenic pollen spreading throughout the environment, thereby eliminating possible crosses with wild plant species or other non-transgenic crops. The combination of a desired transgene flanked on both sites by different male-sterility inducing overexpressing genes would decrease the frequency of pollen formation to an extremely low level. An example is an overexpressing construct of RKS10 at the 5'end of integrated DNA fragment, the desired transgene expression cassette in the middle and at the 3'end of the integrated DNA the ELS2 overexpressing construct. This complete DNA fragment is integrated into the genome by conventional techniques, like particle bombardment, *Agrobacterium* transformation etc. Another possible application concerns the modification of pollen in ornamental plant species like lily, where the release of pollen from cut flowers can be avoided by making transgenic plants in which pollen development is initiated by release from the stamen is prevented (a desired trait that can be obtained by overexpressing for example ELS2, resulting in partial pollen development). Hereby the ornamental value of the stamen with pollen is not lost, but release of pollen is inhibited.

30 Results obtained

Overexpression and antisense constructs of full length RKS cDNA clones have been made under the control of 35S promoters. Transgenic plants have been produced in *Arabidopsis thaliana*. Subsequent generations of stably transformed plants were investigated for phenotypes and analyzed in detail. T2 transgenic seedlings of *Arabidopsis* were germinated on MS agar plates without hormones. Control transgenic plants

containing a negative control vector pGreen4K (empty expression vector) were included as references for normal stamen and pollen development. RKS10 and ELS2 resulted in sterile plants when overexpressed in *Arabidopsis*. Antisense RKS10 plants resulted in a strong reduction in the number of pollen formed (Figure 36). In order to determine whether pollen development itself was the reason for sterility (and not a combination of pollen developmental mutants coupled to either embryo lethals or female gametogenesis defects), reciprocal crosses were performed between sterile transgenic plants and wildtype *Arabidopsis thaliana* WS plants. These results confirmed that the sterile plants with overexpressing RKS10 and ELS2 constructs were male sterile but completely female fertile. No defects could be observed in embryo development from crosses between female transgenic overexpressors and male wildtype pollen (results not shown). Since both antisense and overexpressing constructs of the RKS10 gene showed defects in proper pollen development we conclude that normal levels of endogenous RKS10 gene product are essential for proper pollen formation, outgrowth and differentiation. In the ELS2 overexpressing plants the initiation of pollen grains was not inhibited. However the proper development of pollen grains in full grown viable pollen was clearly inhibited .

25

Literature

- The *Arabidopsis* male sterility1 (MS1) gene is a transcriptional regulator of male gametogenesis, with homology to the PHD-finger family of transcription factors. Wilson et al. 2001. the Plant Journal 28: 27-39
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35

8. Resistance mechanisms

Two-hybrid interaction experiments have already shown *in vitro* interaction between RKS and NDR0-NHL and members of the SBP/SPL family. Here we show that *in vivo* the individual components of this signalling cascade are regulating identical processes, as based on functional genomics on transgenics plants, overexpressing or co-suppressing single components or combinations of components in this transmembrane signalling complex.

Here we show a large number of new members of the NDR/NHL gene family and we postulate a function as syntaxins in the pathogen resistance:

- 15 **At2g27080;**
 MAERVYPADS PPQSGQFSGN FSSGEFPKKP APPPSTYVIQ VPKDQIYRIP PPENAHRFEQ
 LSRKKTNRSN CRCCFCFLA AVFILIVLAG ISFAVLYLIY RPEAPKYSIE GFSVSGINLN
 STSPISPSFN VTVRSRNGNG KIGVYEEKES SVDVYNDVD ISNGVMPVYF QPAKNVTVVK
 LVLSGSKIQL TSGMRKEMRN EVSKKTVPFK LKIKAPVKIK FGSVKTWTMI VNVD CDVTVD
 20 KLTAPSRIVS RKCSHDVDLW ****** (SEQ ID NO: 66)
- At5g21130**
 MTVEKPQEMT GDTNSDGFLT NKDVHRIKHP SLDTNDSSSS RYSVDSQKSR IGPPPGTYVI
 KLPKDQIYRV PPPENAHRYE YLSRRKTNKS
 25 CCRRCLCYSL SALLIIIVLA AIAFGFFYLV
 YQPHKPQFSV SGVSVTGINL TSSSPFSPVI RIKLRSQNVK GKLGLIYEKG NEADVFFNGT
 KLGNGEFTAF KQPAGNVTVI VTLKGSSVK LKSSSRKELT ESQKKGKVPF GLRIKAPVKF
 KVGSVTTWTM TITVDCKITV DKLTASATVK TENCETGLSL **L*** (SEQ ID NO: 67)
- 30 **At1g65690**
 MSQHQQIYPV QDPEAATARP TAPLVPRGSS RSEHGDPKSV PLNQRQRFV PLAPPKRRS
 CCCRCFCYTF CFLLLLVAV GASIGILYLV FKPCLPDYSI DRLQLTRFAL NQDSSLTTAF
 NVTITAKNPV EKIGIYYEDG SKITVWYMEH QLSNGSLPKF YQGHENTTVI YVENTGQTQN
 ASGLRTTLEE QQRTGNIPV RIRVNQPVV KFGKLKLFV RFLVRCGVFV DSLATNNVIK
 35 IQSSSCKFRL **RL*** (SEQ ID NO: 68)
- At5g36970**
 MSDHQKIHPV SDPEAPPHT APLVPRGSSR SEHGDPKTKQ QAAPLDPPRE KKGSR
 CWCRCVCYTLVLF LLIVIVGAIV GILYLVFRPK FPDYNIDRLQ LTRFQLNQL
 40 SLSTAFNVTI
 TAKNPNEKIG IYYEDGSKIS VLYMQTRISN GSLPKFYQGH ENTTIILVEM TGFTQNTATSL
 MTTLQEQQL TGSIPLRIRV TQPVRIKLGK LKLMKVRFLV RCGVSVDLSA ANSVIRVRSS
 NCKYRFRL* (SEQ ID NO: 69)
- 45 **At1g54540**
 MGDQQKIHPV LQMEANKTKT TTPAPGKTVL LPVQRPIPPP VIPSKNRNMC CKIFCWLSSL
 LVIALIALAI AVAVVYFVVFH PKLPSYEVNS LRVTNLGINL DLSLSAEFKV EITARNPNEK
 IGIYYEKGGH IGVWYDKTKL CEGPIPRFYQ GHRNVTKLVN ALTGRAQYGN TVLAALQQQQ
 QTGRVPLDLK VNAPVAIKLG NLKMKKIRIL GSCKLVVDSL STNNNINIK SDCSFKAKL* (SEQ ID NO: 70)
 50 **At5g06320**

MADLNGAYYG PSIPPPKKVS HSHGRRGGGC GCLGDCLGCC GCCILSVIFN ILITIAVLLG
IAALIIWLIF RPNAIKFHVT DAKLTEFTLD PTNNLRYNLD LNFTIRNPNR RIGVYDEIE
VRGYYGQDRF GMSNNISKFY QGHKNTTVVG TKLVGQQLVL LDGGERKDLN EDVNSQIYRI
DAKLRLKIRF KFGLIKSWRF KPKIKCDLKV PLTSNSTSGF VFQPTKCDVD F** (SEQ ID NO: 71)

5

At5g11890

MTDRVFPASK PPTATNGAPP VGSIPPPAP ATVTSNGTTN GMANQKPQVY IPANRPVYRP
QPYSRRHHHQ SRPSCRRICC CCCFWSILII LILALMTAIA ATAMYVIYHP RPPSFVSPTI
RISRVLNLTTS SDSSVSHLSS FNFNLTISEN PNQHLFSFYD PFTVTVNSAK SGTMLNGCTV
10 PAFFSDNGNK TSFHGVIATS TAARELDPDE AKHLRSDLTR ARVGYEIEMR TKVKMIMGKL
KSEGVBIKVT CEGFEGTIPK GKTPIVATSK KTKCKSDLSV KVKWSF* (SEQ ID NO: 72)

At1g17620

MTDDRVPYAS KPPAIVGGGA PTTNPTFPAN KAQLYNANRP AYRPPAGRRR TSHTRG
15 CCCRCCCWTIFVII LLLLVAAAS AVVYLIYRPQ RPSFTVSELK ISTLNFTSAV
RLTTAISLSV
IARNPNKNVG FIYDVTIDITL YKASTGGDDD VVIGKGTIAA FSHGKKNTTT LRSTIGSPPD
ELDEISAGKL KGDLLAKKAV AIKIVLNSKV KVMGALKTP KSGIRVTCEG IKVVAPTGKK
ATTATTSAK CKVDPRFKIW KITF** (SEQ ID NO: 73)

20

At3g11650

MGSKQPYLNG AYYGPSIPPP PKAHRSYNSP GFGCCCFSCS GSCLRCCGCC ILSLICNILI
AVAVILGVAA LILWLIFRPN AVKFYVADAN LNRFSFDPNN NLHYSLDLNF TIRNPNQVRG
25 VYDEFSVSG YYGDRFGSA NVSSFYQGHK NTTVILTKE GQNLVVLGDG ARTDLKDEK
SGIYRINAKL RLSVRPKFWF IKSWKLKPKI KCDDLKIPLG SSNSTGGFKF QPVQCFDLS** (SEQ ID NO: 74)

At2g22180

MEGPRRPPSA TAPDSDDDKP DDPPSVWHRP TSSLPALPSL DPPSHGSHHW RNHSLNLSPL
30 PTTSSPPLPP PDSIPELETY VVQVPRDQVY WTPPPEHAKY VEKRSKNPEK NKKKGCSKRL
LWFFIILVIF GFLLGAILLI LHFAFNPTLP VFAVERLTVN PSNFEVTLRA ENFTSNMGVR
YMEKNGVVS LTYKNKSLGS GKFPGLSQAA SGSDKVNKVL NGSTKNAVVO PRGSKQPVVL
MLNMEKAEY EAGPVKRNKE VVVTCDVKVK GLLDAKKVEI VSENCESEFK N* (SEQ ID NO: 75)

35

At5g22870

MCHKPKLELM PMETSPAQPL RRPSLICYIF LVILTILFMA AVGFLITWLE TKPKKLRYTV
ENASVQNFNL TNDNHSATF QFTIQSHNPN HRISVYSSV EIFVKFKDQT LAFDTVEPFH
QPRMNVKQID ETLIAENVAV SKSNGKDLRS QNSLGKIGFE VFVKARVRPK VGIWKSSHRT
40 AKIKCSHVTV SLSQPNKSQN SSCDADI* (SEQ ID NO: 76)

At2g35980

MAABQPLNGA FYGSPVPPPA PKGYRRGHG RGCGCCLLSL FVKVIISLIV ILGVAALIFW
LIVRPRAIKF HVTDASLTRF DHTSPDNILR YNLALTVPVR NPNKRIGLYY DRIEHAHAYE
GKRFTITLIT PFYQGHKNTT VLTPTFQGGN LVIFNAGQSR TLNAERISGV YNIEIKFRLR
45 VRFKLGDLKF RRIKPKVDCD DLRLPLSTSN GTTTTSTVFP IKCDFDF** (SEQ ID NO: 77)

At2g46300

MADYQMNPNV QKPPGYRDPN MSSPPPPPPP IQQQPMRKAV PMPTSYPKK KRRSCCRFCC
CCICITLVLF IFLLLVGTAV FYLWFDPKLP TFSLSASRLD GFKLADDPDG ASLSATAVAR
50 VEMKNPNKSL VFYNGNTAVD LSVGSGNDET GMGETTMNGF RQGPKNSTSV KVETTVKNQL
VERGLAKRLA AKFQSKDLVI NVVAKTKVGL GVGGIKIGML AVNLRCCGVS LNKLDTDSPK
CILNTLKWYK IISN* (SEQ ID NO: 78)

At4g05220

55 MTPDRTTIPI RTSPVPRAQP MKRHHSASY AHRVRESLST RISKFICAMF
LLVLFFVGVVI AFILWLSLRP HRPRFHIQDF

VVQGLDQPTG VENARIAFNV TILNPNQHMG VYFDSMEGSI YYKDQRVGLI
 PLLNPFQOP TINTIVTGTL TGASLTVNSN RWTEFSNDRA QGTVGFRLLDI
 VSTIRFKLHR WISKHHRMHA NCNIVVGRDG LILPKFNHHR CPVYFT* (SEQ ID NO: 79)

5 **At2g35460**
 MANGLINGASY GPPIKPPVKT YYSHGRRGSD VCGGICGCFS SCLLCCGGCL VNIICNILIG
 VLVCLGVVAL ILWFILRPNV VKFQVTEADL TRFEFDPRSH NLHYNISLNF SIRNPNQRLG
 IHYDQLEVRG YYGDQRFSA NMTSFYQGHK NTTVVGTELN GQKLVLGAG GRRDFREDRR
 SGVYRIDVKL RFKLRPFKGF LNSWAVRPKI KCHLKVPLST SSSDERFQFH PTKCHVDL* (SEQ ID NO: 80)

10 **At2g27260**
 MQDPSRPATG YPYPPYPNP QQQQPPTNGY PNPAAGTAYP YQNHNPYYAP QPNPRAVIIR
 RLFIIVFTTL LLLGLILFIF FLIVRPQLPD VNLNSLSVSN FNVSNQVSG KWDLQLQFRN
 PMSKMSLHYE TALCAMYNNR VSLSETRLQP FDQGGKQTV VNATLSVSGT YVDGRLVDSI
 15 GKERSVKGNV EFDLRMISYV TFRYGAFRRR RYVTVCDDV AVGVVPSSGE GKMVGSSKRC
 KTY** (SEQ ID NO: 81)

At4g01410
 MGEGEAKAEH AAKADHKNA SASSTPESYS KEGGGGGGDA RRAICGAIFT ILVILGIAL
 20 ILWLIVRPHK PRLTVVGA AI YDLNFTAPPL ISTSVQFSVL ARNPNRRVSI HYDKLSMYVT
 YKQDIITPPL PLPPLRLGHK STVVIAPVMG GNGIPVSPEV ANGLKNDEAY GVVLMRVVIF
 GRLRWKAGAI KTGRYGFYAR CDVWLRFPNS SNGQVPLAP STCKVDV* (SEQ ID NO: 82)

At5g22200
 25 MTGRYCDQHN GYEERRMRMM MRRIAWACLG LIVAVAFVVF LVWAILHPHG PRFVLQDVTT
 NDFNVSQPNF LSSNLQVTVS SRNPNDKIGI FYDRLDIYVT YRNQEVTLAR LLPSTYQGH
 EVTWVSPFLI GSAVPVAPYL SSALNEDLFA GLVLLNIKID GWVRWKVGSW VSGSYRLHVN
 CPAFITVTGK LTGTGPAIKY QLVQRCADV * (SEQ ID NO: 83)

30 **At1g61760**
 MHNKVDSPV RSNPSTRPIS RHHSASNIVH RVKESLTRV SKLCAIFLS LLLCLGIITF
 ILWISLQPHR PRVHIRGFSI SGLSRPDGFE TSHISFKITA HNPQNNGIY YDSMEGVSYY
 KEKRIGSTKL TNPFYQDPKN TSSIDGALS PAMAVNKDRW MEMERDRNQG KIMFRLKVR
 MIRFKVYTW H SKSHKMYASC YIEIGWDGML LSATKDKRCP VYFT* (SEQ ID NO: 84)

35 **At3g52470**
 MSKDCGNHGG GKEVVVRKLC AAIIFIVIV LITIFLVWVI LRPTKPRFVL QDATVYAFNL
 SQPNLLTSNF QVTIASRNP SKIGIYYDRL HVIATYMNQ ITLRTAIPPT YQGHKEVNVW
 SPFVYGTAVP IAPYNSVALG EEKDRGFVGL MIRADGTVRW KVRTLITGKY HIHVRCAFI
 40 NLGKAAGVL VGDNAVKYTL ANKCSVNV** (SEQ ID NO: 85)

At5g53730
 MSQISITSPK HCAKKGGINI NNRHKKLFFT FSTFFSGLLL IIFLVWLILH PERPEFSLTE
 ADIYSLNLT STHLLNSSV QLTLSKNPN KKVGIYDKL LVYAAYRGQQ ITSEASLPPF
 45 YQSHEEINLL TAFLLQGTLP VAQSFGYQIS RERSTGKIII GMKMDGKLW KIGTWVSGAY
 RFNVNCLAIV AFGNMNMTTP LASLQGTRCS TTI* (SEQ ID NO: 86)

At4g01110
 MAGETLLKPV LQKPPGYREL HSQPQTPLGS SSSSSSMLRR PPKHAIPAAF YPTKKRQWSR
 50 CRVFCVCVCI TVAIVILLI LTVSVFFLYY SPRLPVVRLS SFRVSNFNFS GKGAGDGLSQ
 LTAEATARLD FRNPNGKLRY YYGNVDVAVS VGEDDFETSL GSTKVKGFE KPGNRTVVIV
 PIKVKKQQVD DPTVKRLRAD MKSKKLVVKV MAKTGVGLGV GRRKIVTVGV TISCGVRLQ
 TLDSKMSKCT IKMLKWVPI QVKCI* (SEQ ID NO: 87)

55 **At2g35960**
 MTTKDCGNHG GGGGGGTASR ICGVIIGFII IVLITIFLVW IILQPTKPRF ILQDATVYAF

NLSQPNLLTS NFQITIASRN RNSRIGIYYD RLHVYATYRN QQITLRTAIP PTYQGHKEDN
VWSPFVYGN VPIAPFNAVA LGDEQNRGFV TLIIRADGRV RWKVGTLITG KYHLHVRCQA
FINLADKAAG VHVGENAVKY MLINKCSNVV * (SEQ ID NO: 88)

5 **At3g52460**

MPSPPBEETQ PKPDTGPGQN SERDINQPPP PPPQSQPPPP QTQQQTYPPV MGYPGYHQPP
PPYPNYPNAP YQQYPYAQAP PASYYGSSYP AQQNPVYQRP ASSGFVRGIF TGLIVLVVLL
CISTTITWLW LRPQIPLFSV NNFSVSNFNV TGPVFSAQWT ANLTIENTNT KLKGYFDRIQ
GLVYHQNAV G EDEFLATAFF QPVFVETKKS VVIGETLTAG DKEQPKVPSW VVDEMCKERE

10 TGTVTIFSLRM AVWVTFKTDG WAARESGLV FCGKLKVGFE GISNGAVLL PKPLPCVVYV* (SEQ ID NO: 89)

At4g09590

MTTKECGNHG GGGGGGGTAC RICGAIIGFI IIVLMTIFLV WIILOPKNPE FILQDITVYA
FNLSQPNLLT SKFQITIASR NRNSNIGIYY DHLHAYASYR NQQTILASDL PPTYQRHKED
15 SVWSPLLYGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGQ VRWKVGTLTI GNYHLHVRCQ
AFINQADKAA GVHVGENTVK YTLINKCSVN F* (SEQ ID NO: 90)

At2g35970

MTTKECGNHG GGGGGGGTAC RICGAIIGFI IIVLMTIFLV SIILQPKKPE FILQDITVYA
20 FNLSQPNLLT SKFQITIASR NRNSNIGIYY DHLHAYASYR NQQTILASDL PPTYQRHKEN
SVWSPLLYGN QVPIAPFNAV ALGDEQNSGV FTLTICVDGR VRWKVGTLTI GNYHLHVRCQ
AFINQADKAA GVHVGENTVK YTLINKCSVN F* (SEQ ID NO: 91)

At3g26350

25 MSHHHHHHETN PHFARIPSON PHLKSGGAST SQTSSNQPHI PPIPHPKKSH HKTTQPHVPA
PPGILIKTRG RHRENPIQEP KHSVIPVPLS PEERLPFRKT QNSSKRPLLL SPEDNQQRQ
PPPQAPQRNG GYGSTLPPPI PKPSPWRTAP TSPHRRRG PRLPPSRETN AMTWSAAFCC
AIFWVILILG GLIILIVYLV YRPRSPYVDI SAANLNAAYL DMGFLNGDL TILANVTNPS
KKSSVEFSYV TFELYYYNTL IATQYIEPFK VPKKTSMFAN VHLVSSQVQL QATQSRELQR
30 QIETGPVLLN LRGMFARSH IGPLFRYSYK LHTHCSVSLN GPPLGAMRAR RCNTRK* (SEQ ID NO: 92)

At3g11660

MKDCENHGHG RRKLIRRIWF SIIFVLFIIF LTILLIWAII QPSKPRFILQ DATVYAFNVS
GNPPNLLTSN FQITLSSRNP NNKIGIYYDR LDVYATYRSQ QITFPTSIPP TYQGHKDVDI
35 WSPFVYGTSTV PIAPFNGVSL DTDKDNQVVL LIIRADGRVR WKVGTFITGK YHLHVKCPAY
INFGNKANGV IVGDNAVYKT FTTSCSVSV** (SEQ ID NO: 93)

At3g44220

MTEKECEHHH DEDEKMRKRI GALVLGFLAA VLFVFLVWA ILHPHGPRFV
40 LQDATIYAFN VSQPNYLTSN LQVTLSSRNP NDKIGIFYDR LDIYASYRNQ
QVTLATLLPA TYQGHLDVTI WSPFLYGTIV PVAPYFSPAL SQDLTAGMVL
LNIKIDGWVR WKVGTVVSGR YRLHVNCPAY ITLAGHFSGD GPAVKYQLVQ RCAVDV* (SEQ ID NO: 94)

At1g08160

45 MVPPNPAHQP ARRTQPQLQP QSQPRAQPLP GRRMNPVLCI IVALVLLGLL VGLAILITYL
TLRPKRLIYT VEAASVQEFA IGNNDDHINA KFSYVIKSYN PEKHVSRYH SMRISTAHN
QSAHKNISP FKQRPKNETR IETQLVSHV ALSKFNARDL RAEKSKGTIE MEVYITARVS
YKTWIFRSRR RTLKAVCTPV MINVTSSSLD GFQRVLCKTR L** (SEQ ID NO: 95)

50 **At2g01080**

MPPPPSSSRA GLNGDPIAAQ NQQPYRSYS SSSASLKGCC CCLFLLFAF LALLVLAVVL
IVILAVKPKK PQFDLQQVAV VYMGISNPSA VLDPTTASLS LTIRMLFTAV NPNKVGIRYG
ESSFTVMYKG MPLGRATVPG FYQDAHSTKN VEATISVDRV NLMQAAHADL VRDASLNDV
ELTVRGDVG KIRVMNFDSP GVQVLLPSFL PAFCSLSLA * (SEQ ID NO: 96)

55

At5g06330

- MTSKDCGSHD SHSSCNRKIV IWTISIILL ILVVILLVWA ILQPSKPRFV LQDATVFNFN
VSGNPPNLLT SNFQFTLSSR NPNDKIGIYY DRLDVYASYR SQQITLPSPM LTTYQGHKEV
NVWSPFVGGY SVPVAPYNAF YLDQDHSSGA IMLMLHLDGR VRWKVGSFIT GKYHLHVRCH
ALINFGSSAA GVIVGKYMLT ETCSVSV* (SEQ ID NO: 97)
- 5 **At5g56050**
MSKFSPPPQS QPQPPTPPW ETPSSKWYSP IYTPWRTTPR STQSTPTTTP IALTEVIVSK
SPLSNQKSPA TPKLDSMEAH PLHETMVLLQ LRSTRTNPWI WCGAALCFIF SILLIVFGIA
TLILYLAVKP RTPVFDISNA KLNTILFESP VYFNGDMLLQ LNFTNPNNKL NVRFENLMVE
10 LWFADTKIAT QGVLPFSQRN GKTRLEPIRL ISNLVFLPVN HILELRRQVT SNRIAYEIRS
NFRVKAIFGM IHYSYMLHGI CQLQLSSPPA GGLVYRNCTT KRW* (SEQ ID NO: 98)
- At3g20600**
NDR1
15 MNQONEDTEG GRNCTCCLS FIFTAGLTSL FLWLSLRADK PKCSIQNFPI PALGKDPNSR
DNTTLNFMVR CDNPKNKDKGI YYDDVHLNFS TINTTKINSS ALVLVGNVTV PKFYQGHKKK
AKKWGQVKPL NNQTVLRAVL PNGSAVFRD LKTQVRFKIV FWKTKRYGVE VGADVEVNGD
GVKAQKKGIK MKKSDSSFPPL RSSFPISVLM NLLVFFAIR* (SEQ ID NO: 99)
- 20 **At3g54200**
MSDFSIPDD KKEEEKPATA MLPPPKPNAS SMETQSANTG TAKKLRRKRN CKICICFTIL
LILLIAIVIV ILAFTLFKPK RPTTTIDSVT VDRLOASVNP LLLKVLLNLT LNVDSLKNP
NRIGFSYDSS SALLNYRGQV IGEAPLPANR IAARKTVPLN ITLTLMDRL LSETQLLSDV
MAGVIPLNTF VKVTGKVTVL KIFKIKVQSS SSCDLSISVS DRNVTSQHCK YSTKL* (SEQ ID NO: 100)
- 25 **At3g20590**
non-race specific disease resistance protein, putative
MTKIDPEEL GRKCTCFEK FIFTTRLGAL ILWLSLRACK PKCSIQNFYI PALSKNLSSR
DNTTLNFMVR CDNPKNKDKGI YYDDVHLTFS TINTTTTNS DLVLVANYTV PKFYQGHKKK
30 AKKWGQVWPL NNQTVLRAVL PNGSAVFRD LKTHVRFKIV FWKTKWYRI KVGADVEVNG
DGVKAQKKGS KTKKSDSSLP LRSSFPPIFVL MNLLVFFAIR * (SEQ ID NO: 101)
- At4g39740**
MSHVTATSLA RFTKVPKPA SSPIVNTKLT TSGGRTAAFM DLSSFRITVW
35 DPTDANDSSG KFPWPRFLFF FLTLKTGGSG LNIKPTISAI AQMMNPMTIT
EMNNQMRLE QKLLFLPGS LFLRLSTILH YPEGSNRPD PLEHALRRSR
SLGLDQEEAA KKVIRVGRDS KNDYVNVVEN QAASFLRRCG PSKRIQSVNY
CKSTRQGHEI PDVKPLFPTG GGTQAPSRSR ARYAVPAILL GFAGFVGFLH
YNDERRAVPR QOASSNSGCG CGSNTTVKGP IIGGPFTLVS TENKIVTEND
40 FCGKWVLLYF GYSFSPDVGP BQLKMMKAV DKLAILLNPL TFGCLYLYAE
FDSRILGLTG TASAMRQMAQ EYRVYFKKVQ EDGEDYLVDT SHNMYLINPK
MEIVRCFGVE YNPDELSQEL LKEVASVSQ* (SEQ ID NO: 102)
- At1g32270 syntaxin, putative**
45 MVRSDNVKFQ VYDAELTHFD LESNNNLQYS LSLNLSIRNS KSSIGIHYDR
FEATVYYMNQ RLGAVPMPLE YLGSKNTMLL RALFEGQTLV LLKGNERKKF
EDDQKTGVYR IDVKLSINFR VMVLHLVTWP MKPVVRCHLK IPLALGSSNS
TGGHKKMLLI GQLVKDTSAN LREASETDHR RDVAQSKKIA DAKLAKDFEA
ALKEFQKAQH ITVERETSYI PFDPKGSFSS SEVDIGYDRS QEQRVLMESR
50 RQEIIVLLDNE ISLINEARIEA REQGIQEVKH QISEVMEMFK DLAVMVDHQQ
TIDDIDEKID NLRSAQAQK SHLVKASNTQ GSNSSLLFSC SLLFFFLSG
DLCRCVCVGS ENPRLNPTRR KAWCEEEDEE QRKKQKKKT MSEKRRREEK
KVKNKNGFVF CVLGHK* (SEQ ID NO: 103)
- 55 **At1g13050**

- MSHHHYETNP HFVQFSLQDQ HQGGPSSSWN SPHHHQIPQA HSVAPPRVKI KTRGRHQTEP
 PETIHESFSS RPLPLRPEEP LPPRHNPNSA RPLQLSPPEEQ RPPHRGYGSE PTPWRRAPTR
 PAYQQGPKRT KPMTLPATIC CAILLIVLIL SGLILLLVYL ANRPRSPYFD ISAATLNTAN
 LDMGYVLNGD LAVVNFNTP SKKSSVDFSY VMFELYFYNT LIATEHIEPF IVPKGMSMFT
 5 SFHLVSSQVQ IQMIQSQDLQ LQLGTGPVLL NLRGTFHARS NLGSLMRYSY WLHTQCSISL
 NTPPAGTMRA RRCNTRK* (SEQ ID NO: 104)
- At5g45320**
 MPRLTSRHGT SPFIWCAAI CAIISIVVIV GGIIVFVGYL VIHPRVPIIS
 10 VADAHLDLFLK YDIVGVLTQ LTIVIRVEND NAKAHALFDE TEFKLSYEGK
 PIAILKAPEF EVVKEKSMFL PYLVQSYPIP LNPTMMQAVD YAVKKDVITF
 ELKGGSRTRW RVGPLGSVKF ECNLSCQLRF RPSDHSYIPS PCTSAKH* (SEQ ID NO: 105)
- At3g20610**
 15 MDRDDAWEFV VTIVGSLMTL LYVSFLLALC LWLSTLVHHI PRCSIHYFYI PALNKSLSIS
 DNTTLNFMVR LKNINAKQGI YYEDLHLSFS TRINNSSLV ANYTVPRFYQ GHEKKAKKWG
 QALPFNNQTV IQAVLPNGSA IFRVDLKMV KYKVMWKT RYKLKASVNL EVNEDGATKV
 KDKEDGIMK ISDSSPQRLT FFQVCFSIIC VLMNWLIFLA IR* (SEQ ID NO: 106)
- At4g26490**
 20 MVLTKPATVR FNGLDAEPRK DRVILRQPRS SRTSLWIWCV AVFLAIRPRI PVFDIPNANL
 HTIYFDTPF FNGDLSMLVN FTNPNKKIEV KFEKLRIELF FENRLIAAQV VQPFQKKHE
 TRLEPIRLIS SLVGLPVNHA VELRRQLENN KIEYEIRGT KVAHFGMIH YSYQLHGRCQ
 LQMTGPPTGI LISRNCTTK * (SEQ ID NO: 107)
- At5g42860**
 25 MHAKTDEVT SLSASSPTRS PRRPAYFVQS PSRDSHDGEK TATSFHSTPV
 LTSPMGSPPH SHSSSRFSK INGSKRKGHA GEKQFAMIEE EGLLDDGDRE
 QEALPRRCYV LAFIVGFSLL FAFFSLILYA AAKPQPKIS VKSITFEQLK
 30 VQAGQDAGGI GTDMITMNAT LRMLYRNTGT FFGVHVTSS IDLSFSQITI
 GSGSIKKFYQ SRKSQRTVVV NVLGDKIPLY GSGSTLVPPP PPAPIPKPKK
 KKGPIVIVP PAPPAPVPMR LNFTVRSRAY VLGKLVQPKF YKRIVCLINF
 EHKKLSKHIP ITNNCTVTSI * (SEQ ID NO: 108)
- At1g45688**
 35 MHAKTDEVT SLAASSPARS PRRPVYVQS PSRDSHDGEK TATSFHSTPV LSPMGSPPHS
 HSSMGRHSRE SSSSRFSGSL KPGSRKVNPN DGSKRKGHG EKQWKECAVI EEGLLDDGD
 RDGGVPRRCY VLAIVGFFI LFGFFSLILY GAAKPMKPKI TVKSITFETL KIAGQDAGG
 VGTDMITMNA TLRLYRNTG TFFGVHVTST PIDLSFSQIK IGSGSVKKFY QGRKSERTVL
 40 VHVICEKIPL YGSGSTLLPP APPAPLPKPK KKGAPVPIP DPPAPPAPV MTLFVVRSR
 AYVLGKLVQP KFYKKIECDI NFEHKNLNKH IVITKNCTVT TV* (SEQ ID NO: 109)
- At4g26820**
 45 MDDEQNVEE MNQQLLITVI DTEKVPRLP ISSRSHQESE PANISHWSLL FKLFLAITIM
 GACVAGVTFV ILITPTPTV HVQSMHISFA NNLVPWSAT FSIKNPNEKL HVTYENPSVW
 LVHRGKLVST ARADSFQKG GEKNEVIVKR NETKVIDEEA AWEMEDEVAV TGGVVGLDMV
 FSGRVGFYPG TSALWGEQYM SAVCENSAK LYNVDDEIYG TNRSVLSFDG RLVCVRLPK
 YP* (SEQ ID NO: 110)
- 50

Plants respond in a variety of ways to pathogens. After a recognition of the pathogen, normally mediated by avr and R genes, the resulting response induces a hypersensitive

- response, that results in inhibition of the pathogen. After the recognition, further processes appear to be non-specific. In addition to the hypersensitive response, a second line of defence, defined as the systemic acquired resistance response
- 5 can be triggered, that renders unaffected parts of the plant resistant to a variety of normally virulent pathogens. Several of the RKS and ELS gene products prove to be key regulators in the regulation of the system acquired resistance response.
- 10 Overexpression of several of the RKS and / or ELS genes in plants, either by constitutive promoters, stage and / or tissue specific promoters, or inducible promoters allows the activation of a systemic acquired resistance response in plants.
- 15 Another application can be provided by the activation of a RKS /ELS specific ligand in (transgenic) plants, thereby activating the receptor complex, that finally results in triggered activation of the systemic acquired resistance response in these plants.
- 20 (ref. Generation of broad-spectrum disease resistance by overexpression of an essential regulatory gene in systemic acquired resistance. H. Cao et al. 1998. Proc. Natl. Acad. Sci. USA 95: 6531-6536). Recent literature shows the functional interaction between RKS10 and BRI-1, another class
- 25 of transmembrane LRR receptor kinases (Cell Vol. 110, 213-222 2002). BAK1=RKS10 as described here, interacts with BRI-1 and modulates brassinosteroid signaling; Cell vol 110, 203-212 2002 BRI1/BAK1 a receptor kinase pair mediating brassinosteroid signaling). Brassinosteroids are known to
- 30 function in a broad range of disease resistance in tobacco and rice (Plant Journal 2003, 887-898). The BRI-1 receptor is involved in the binding of systemin, an 18 amino acid polypeptide, representing the primary signal for the systemic activation of defence genes (PNAS 2002, 9585-9590).
- 35 ELS overexpression phenotypes mimic the effects of inactivation of RKS molecules gene products. Either ELS is competing for ligand binding, or ELS inhibits the interactions

between RKS and BRI-1-like gene products. ELS1 overexpression results in dwarf phenotypes in Arabidopsis and tobacco plants, similar as observed for antisense RKS4 and RKS10, and for knock out plants of RKS0 and RKS4.

- 5 Deregulating expression of ELS and / or RKS genes in plant would modify the broad spectrum disease resistance in such plants. This would explain the observed data that brassinosteroids are involved in disease resistance (Plant Journal 2003, 33 887-898.)

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Claims

1. A method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying
5 expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein or encoding a protein comprising a ligand for said complex.
10
2. A method according to claim 1 allowing modulating cellular division during plant growth or organ formation
3. A method according to claim 2 wherein said gene comprises
15 an RKS4 or RKS10 gene or functional equivalent thereof.
4. A method according to claim 1 allowing modulating apical meristem formation.
- 20 5. A method according to claim 4 wherein said gene comprises an ELS1, RKS0, RKS3, RKS4, RKS8 or RKS10 gene or functional equivalent thereof.
6. A method according to claim 4 allowing modulating
25 fasciation.
7. A method according to claim 6 wherein said gene comprises an RKS0, RKS3, RKS8 or RKS10 gene or functional equivalent thereof.
30
8. A method according to claim 4 allowing modulating root development.
9. A method according to claim 7 wherein said gene comprises
35 an ELS1, ELS 2, RKS1, RKS3, RKS4, RKS6, RKS8 or RKS10 gene or functional equivalent thereof.

10. A method according to claim 4 allowing modulating meristem identity.

11. A method according to claim 9 wherein said gene comprises
5 an ELS1, RKS8, RKS10 or RKS13 gene or functional equivalent thereof.

12. A method according to claim 1 allowing modulating pollen development.

10

13. A method according to claim 11 wherein said gene comprises an ELS2 or RKS10 gene or functional equivalent thereof.

15 14. A method for providing resistance to a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising NDR/NHL protein, or encoding a protein comprising a ligand for said complex.

20

15. A method for obtaining a plant or plant cell with a modulated development comprising subjecting a plant or plant cell to a method according to anyone of claims 1 to 13.

25 16. A method for obtaining a resistant plant or plant cell comprising subjecting a plant or plant cell to a method according to claim 14.

17. A plant or plant cell obtainable with a method according
30 to claim 15 or 16.

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- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
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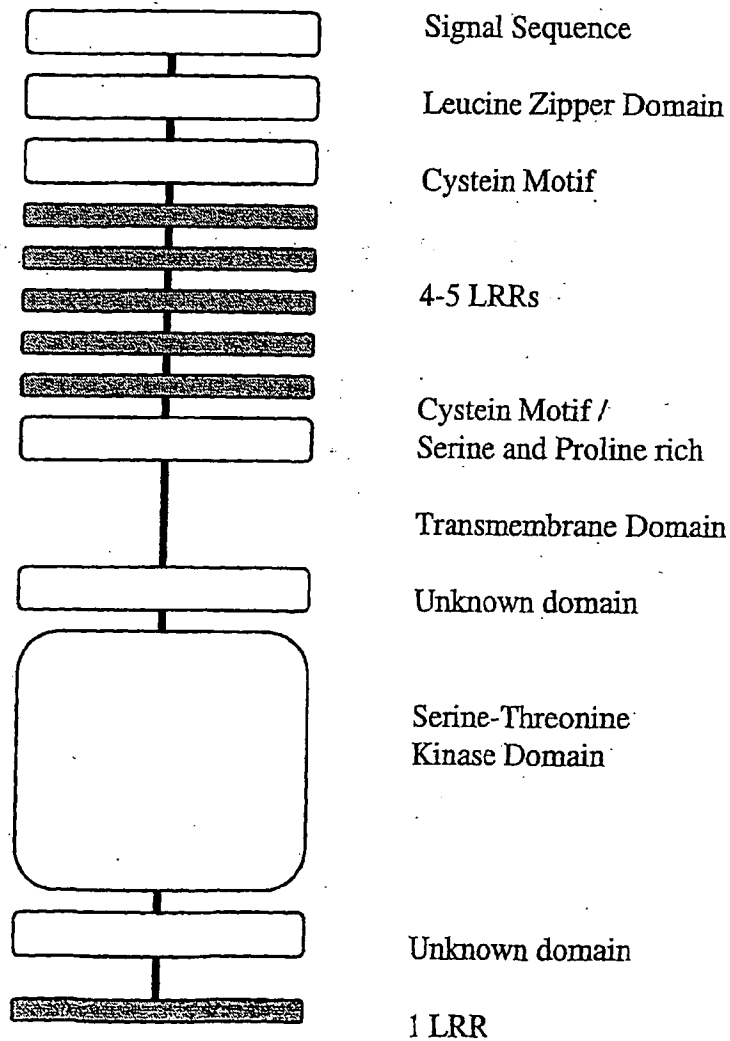
(54) Title: MODULATING DEVELOPMENTAL PATHWAYS IN PLANTS

(57) Abstract: The invention relates to a method to modulate plant growth or development by modifying genes in plants. The invention among others relates to modifying RKS genes or gene products as found in *Arabidopsis thaliana* or other plants. The invention provides a method for modulating a developmental pathway of a plant or plant cell comprising modifying a gene or modifying expression of said gene, wherein said gene is encoding a protein belonging to a signaling complex comprising RKS protein, ELS protein, NDR/NHL protein, SBP/SPL protein and RKS/ELS ligand protein.

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Fig. 1

Different domains of RKS proteins



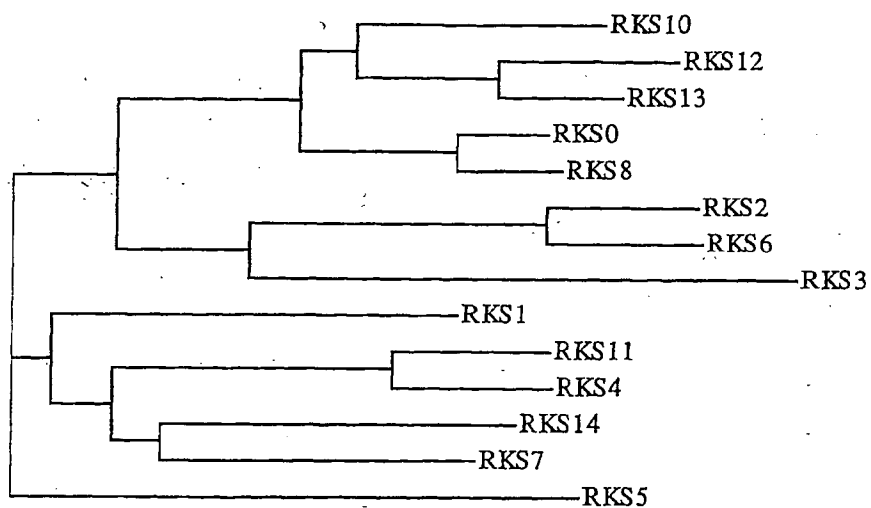
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Fig. 2

Developmental tree of the different Receptor Kinases like SERK (RKS) genes.



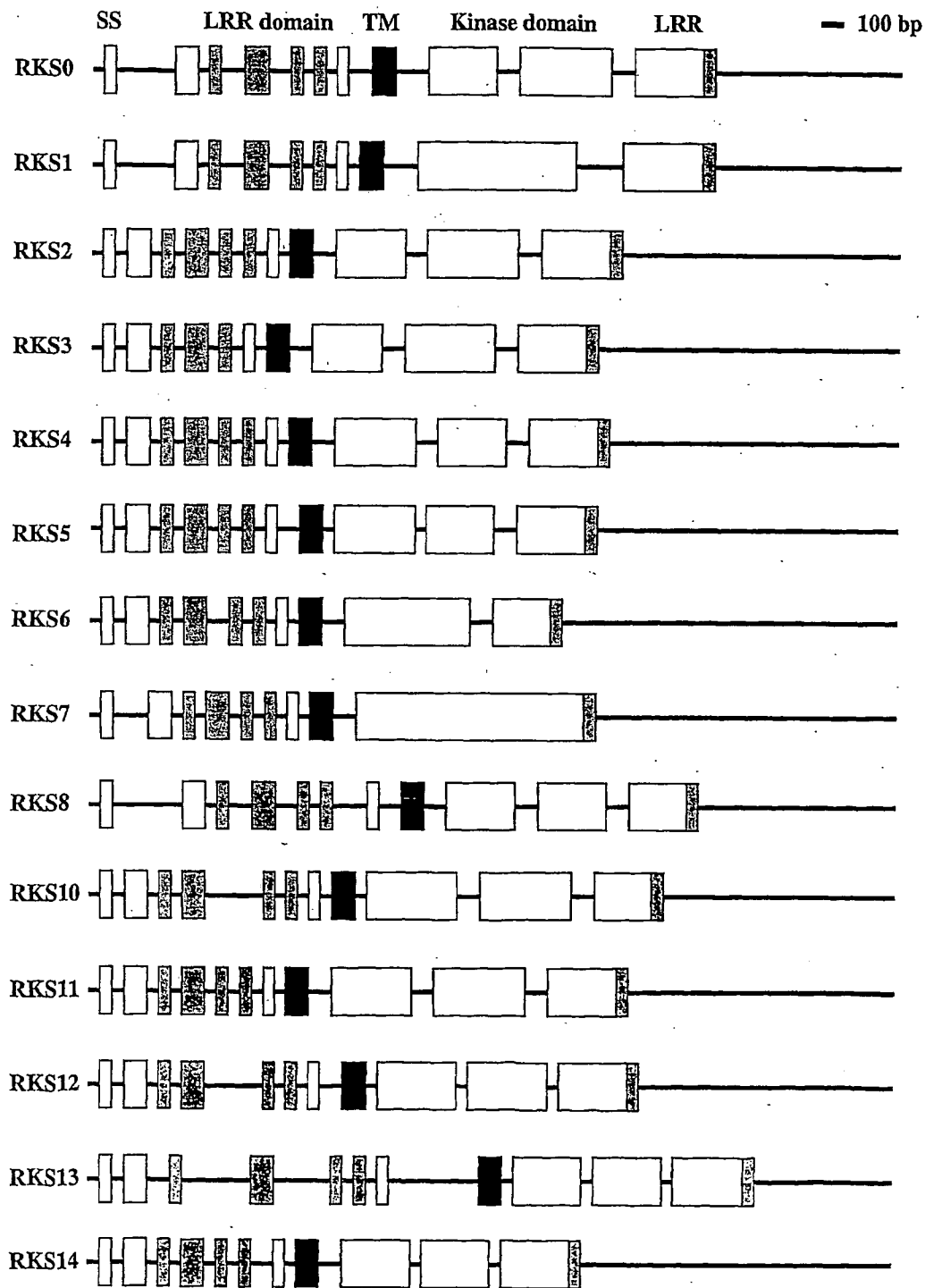
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Fig. 3

Intron-Exon structure of the RKS genes in *Arabidopsis thaliana* var. Columbia.
SS signal sequence; LRR leucine rich repeat domain; TM transmembrane domain.



I
II
III
IV
V

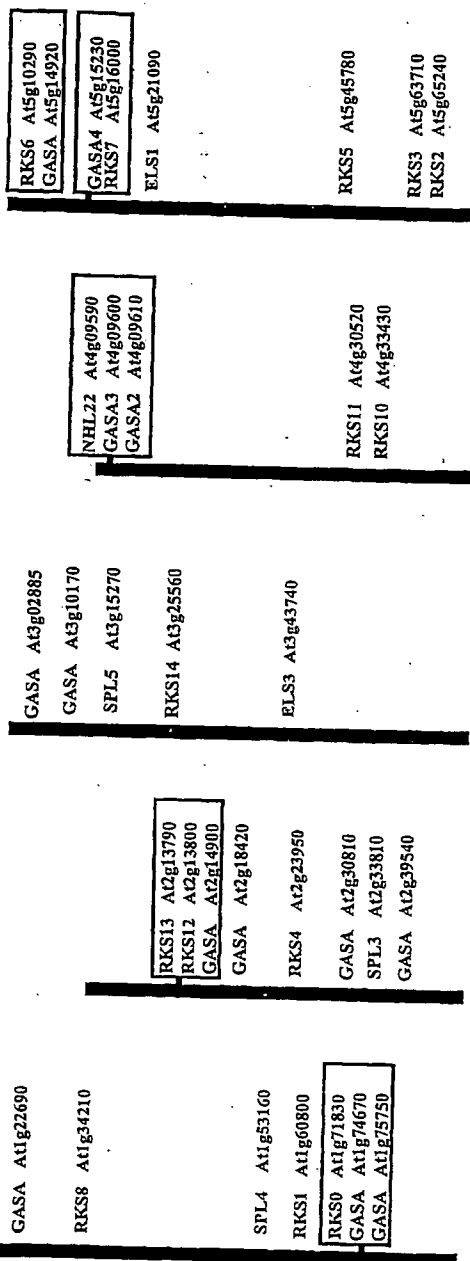
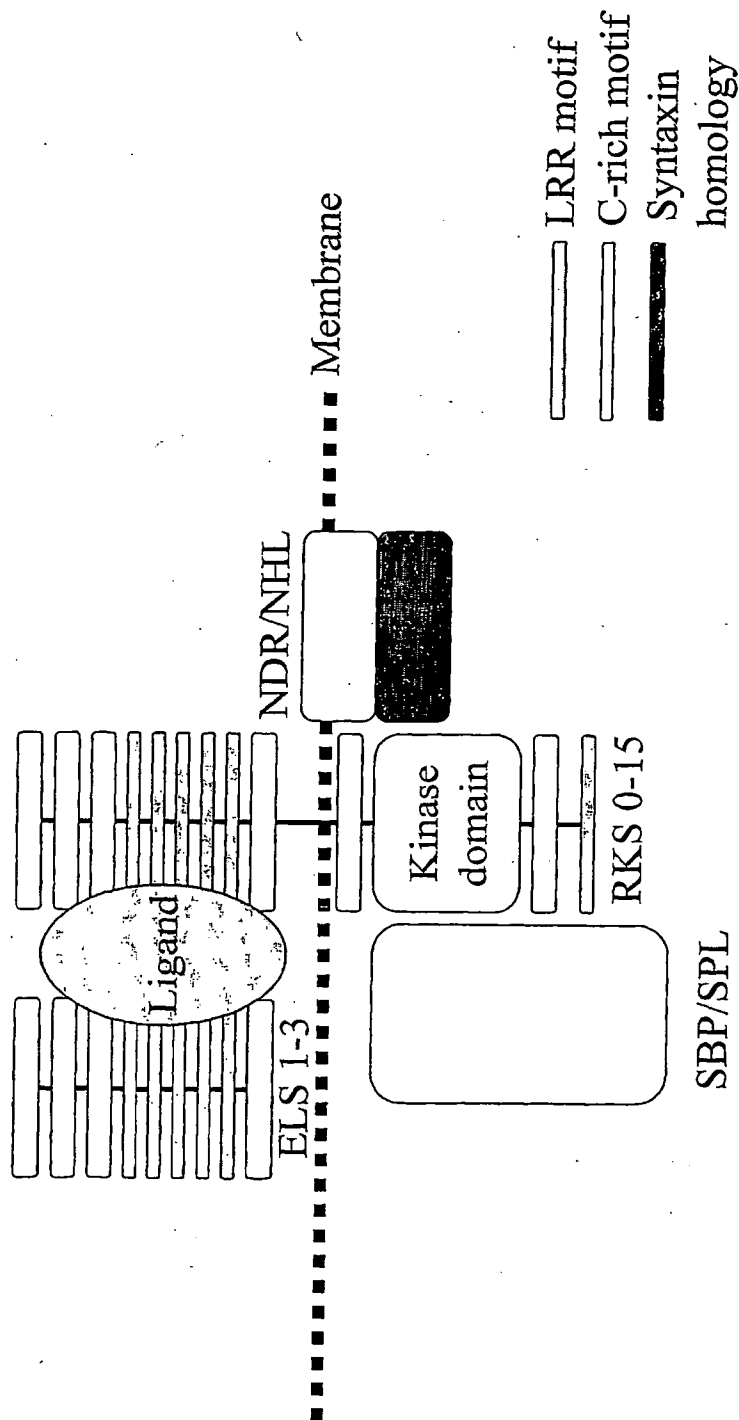


Fig. 5

RKS-mediated signal transduction
 pathway in plants



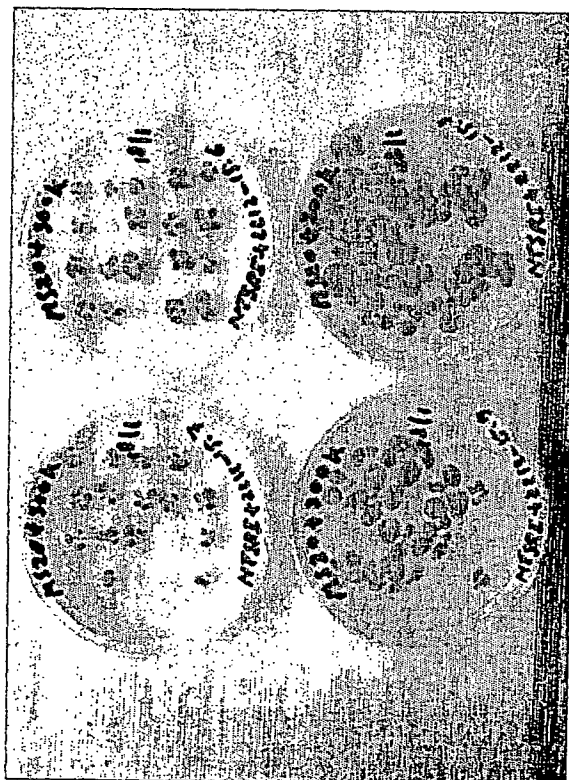
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GT-RKS4 determines seedling size
in *Nicotiana tabacum*.



Modifications in the
expression profile
of GT-RKS4 modulates
organ size within seedlings
of *Nicotiana tabacum*.

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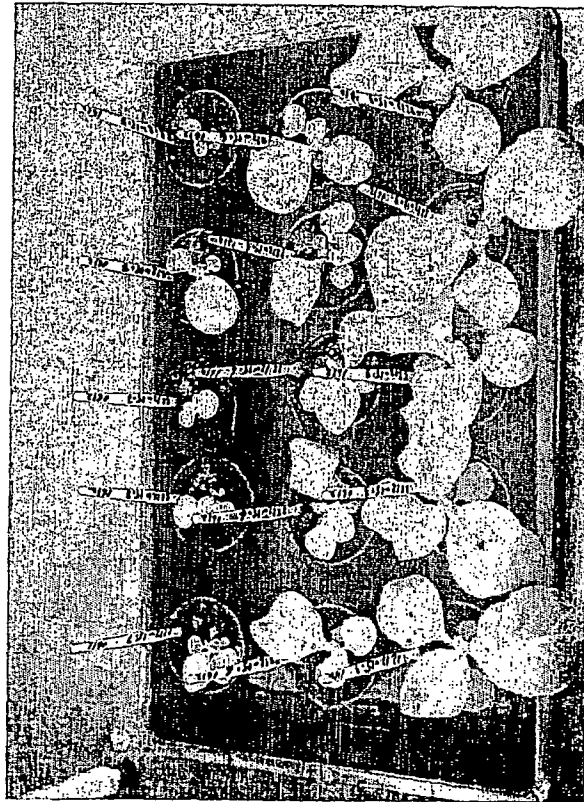
Fig. 7

GT-RKS4-7S-T2

GT-RKS4-6S-T2

GT-RKS4-3S-T2

GT-RKS4 determines organ size
in *Nicotiana tabacum*.



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Fig. 8

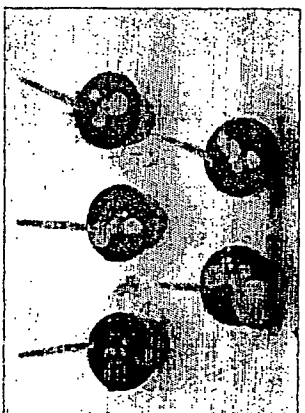
GT-RKS4 determines plant size
in *Nicotiana tabacum*



Empty vector control



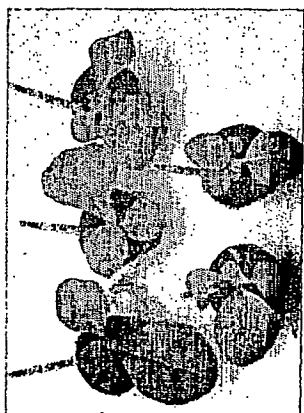
GT-RKS4-15S-6T2



GT-RKS4-15S-7T2



GT-RKS4-15S-3T2

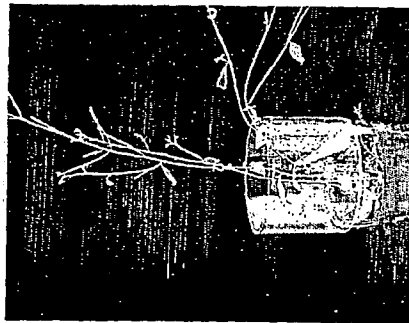


GT-RKS4-15S-9T2

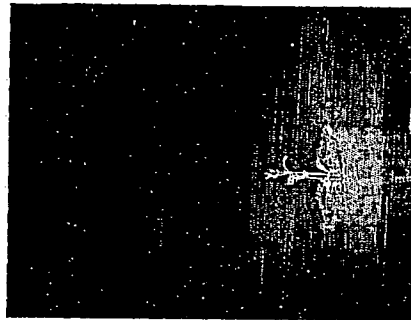
Fig. 9

Stable transformed GT-RKS4-antisense
in *Arabidopsis thaliana*

Wildtype WS



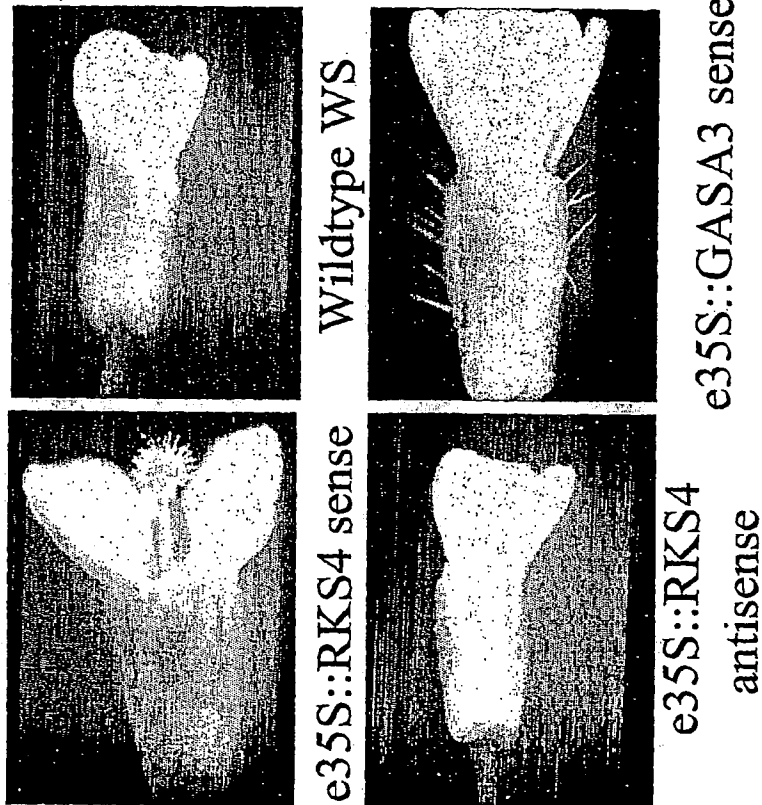
GT-RKS4-16a



Overexpression of antisense GT-RKS4-1a
reduces plant and organ size.

Fig. 10

Ectopic expression of RKS4 and GASA3
gene products both result in increases
flower size in *Arabidopsis thaliana* WS



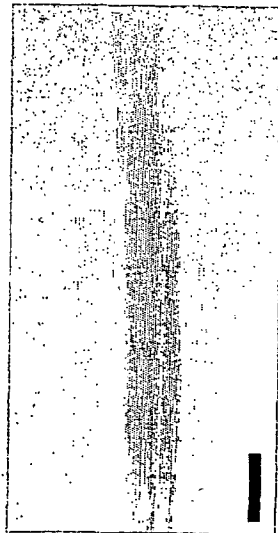
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Fig. 11

Ectopic expression of RKS4 in seedlings results
in the formation of meristematic regions in the
hypocotyl of *Arabidopsis thaliana* WS



pCDG

Destruction

box



CycB1;1

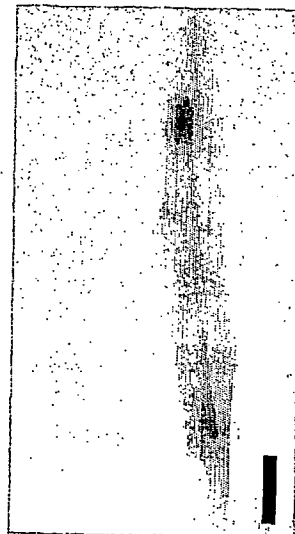


uidA

pCDG

x

e35S::RKS4 sense



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Fig. 12

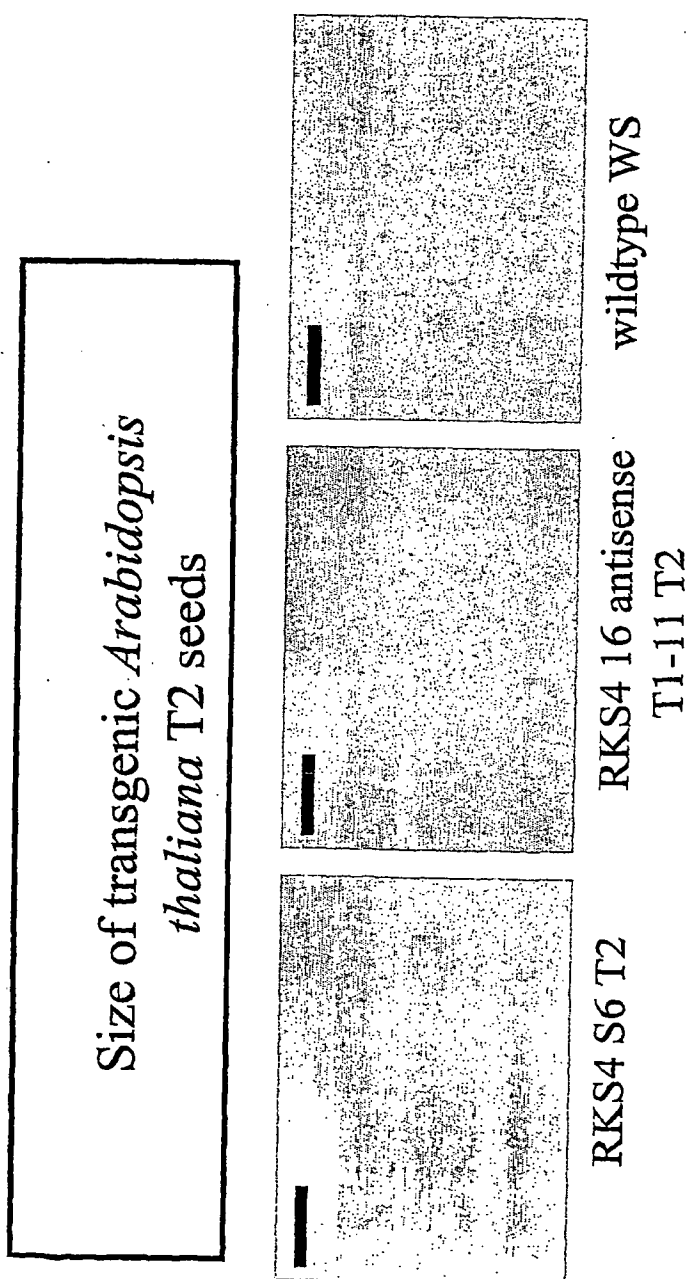


Fig. 13

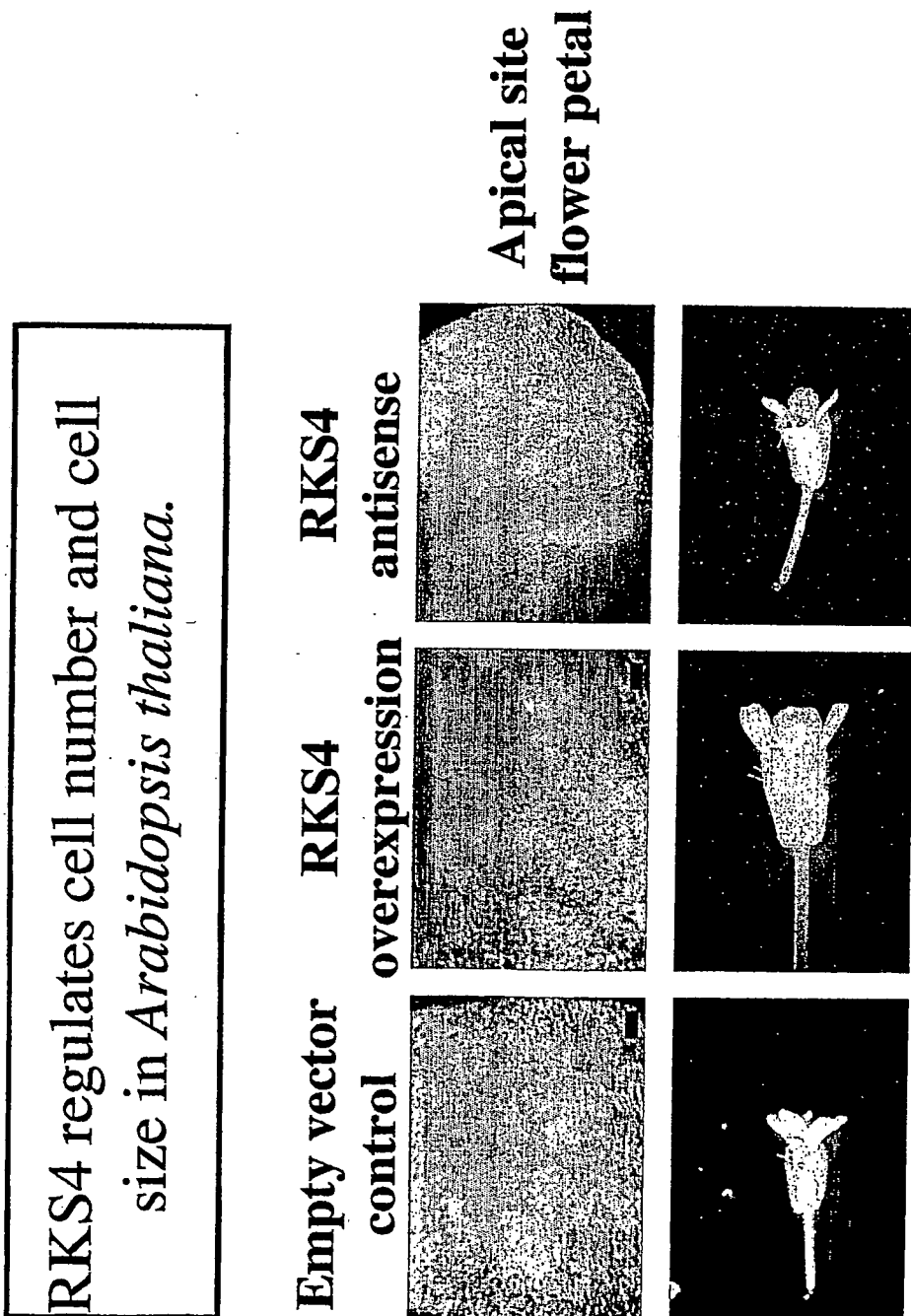
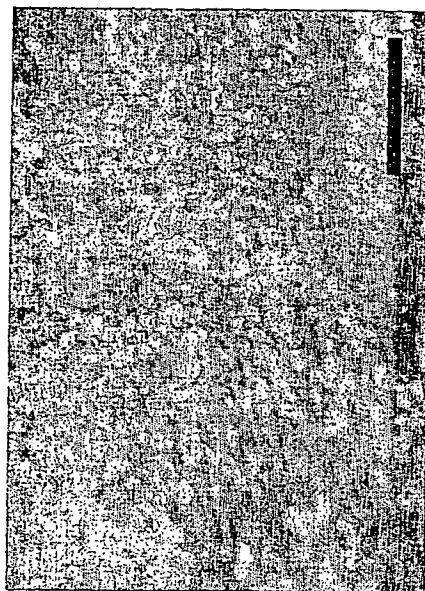
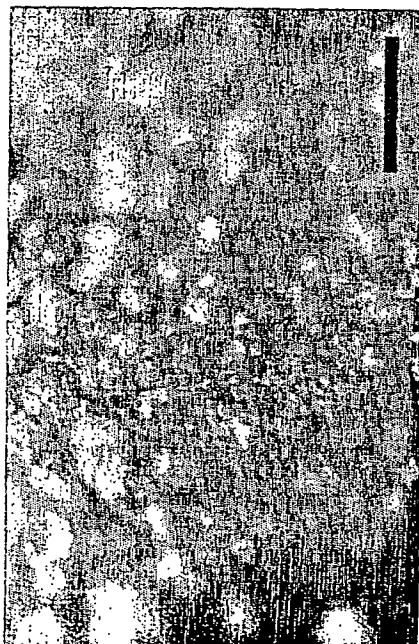


Fig. 14

RKS10S T1-10
results in a decrease in size
of cotyl-like apical epidermal cells



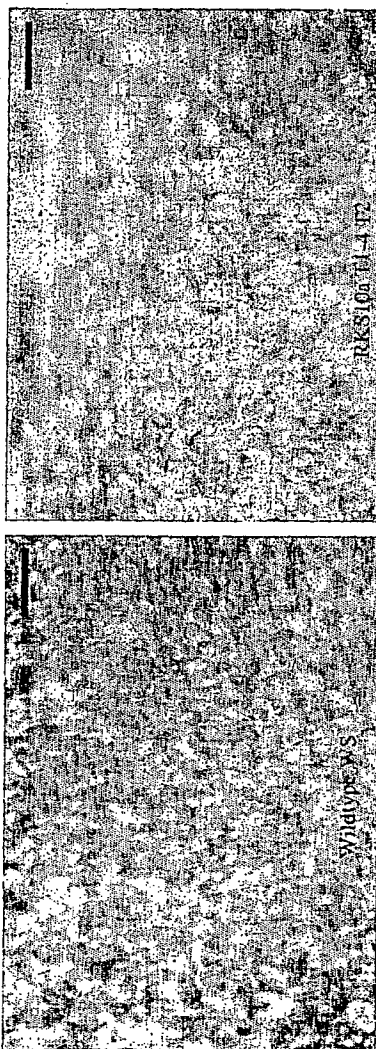
RKS10S T1-10



pGreen 4K

Fig. 15

RKS10antisense T1-4
results in an increase in size
of the cotyl epidermal cells



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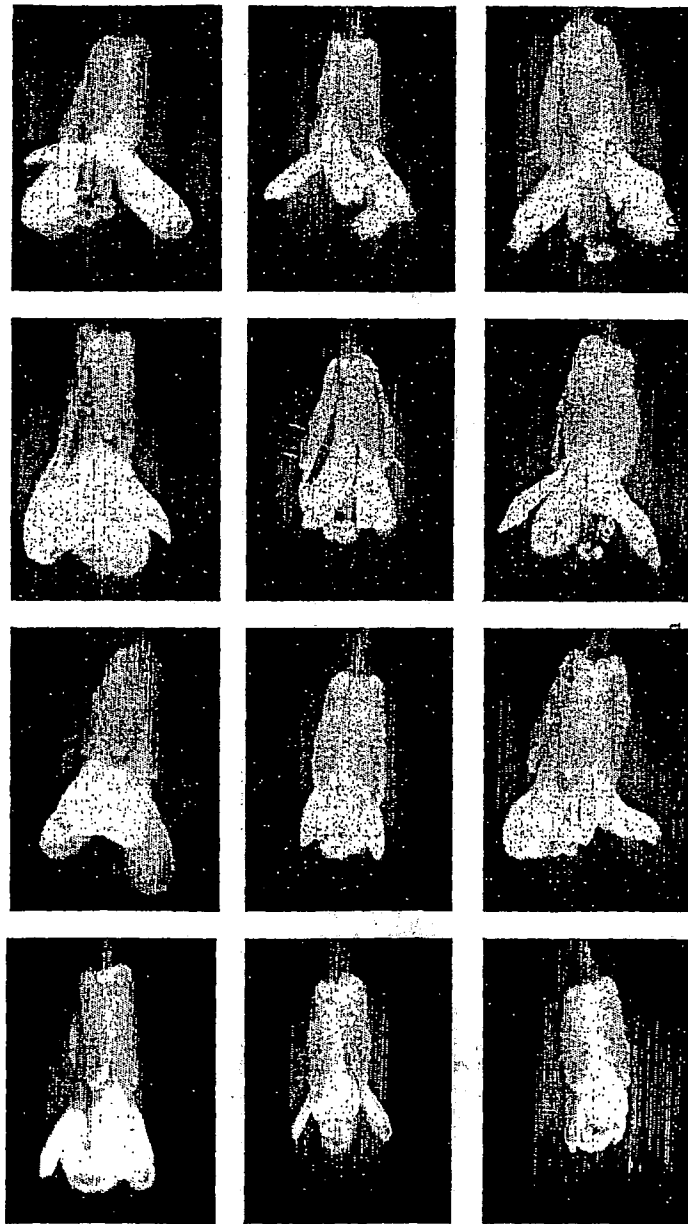
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Fig. 16

Flower development from the same
inflorescence in transgenic
Arabidopsis thaliana



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Fig. 17

Regeneration potential of
Arabidopsis transgenic seedlings.

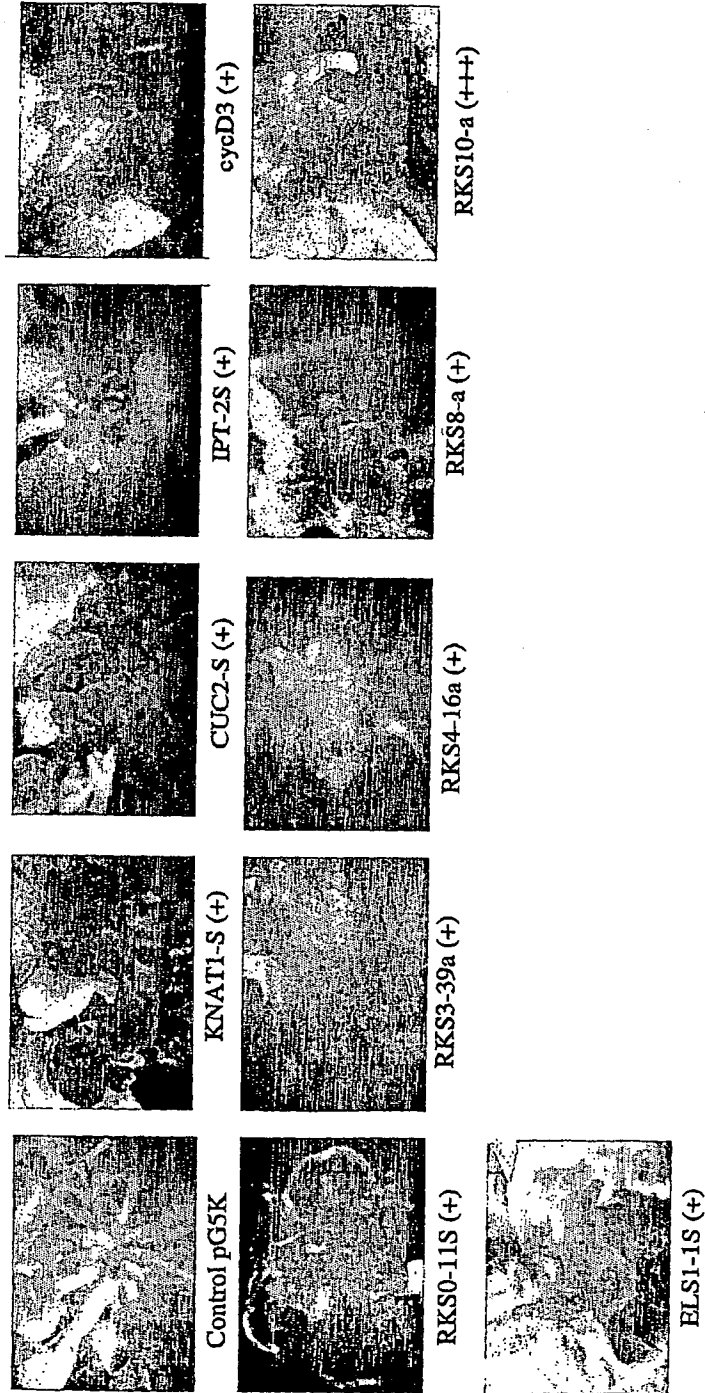
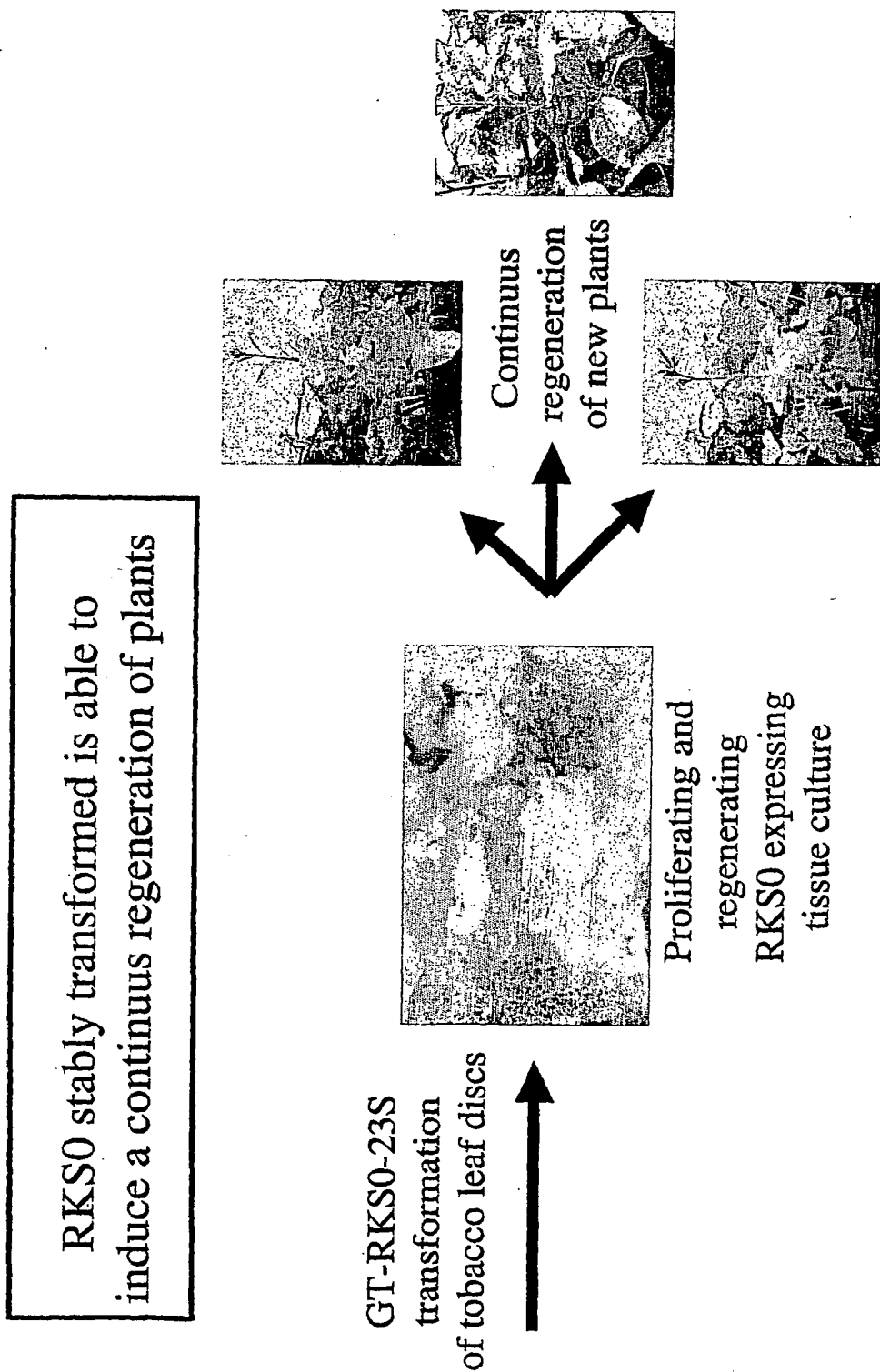


Fig. 18



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Fig. 19

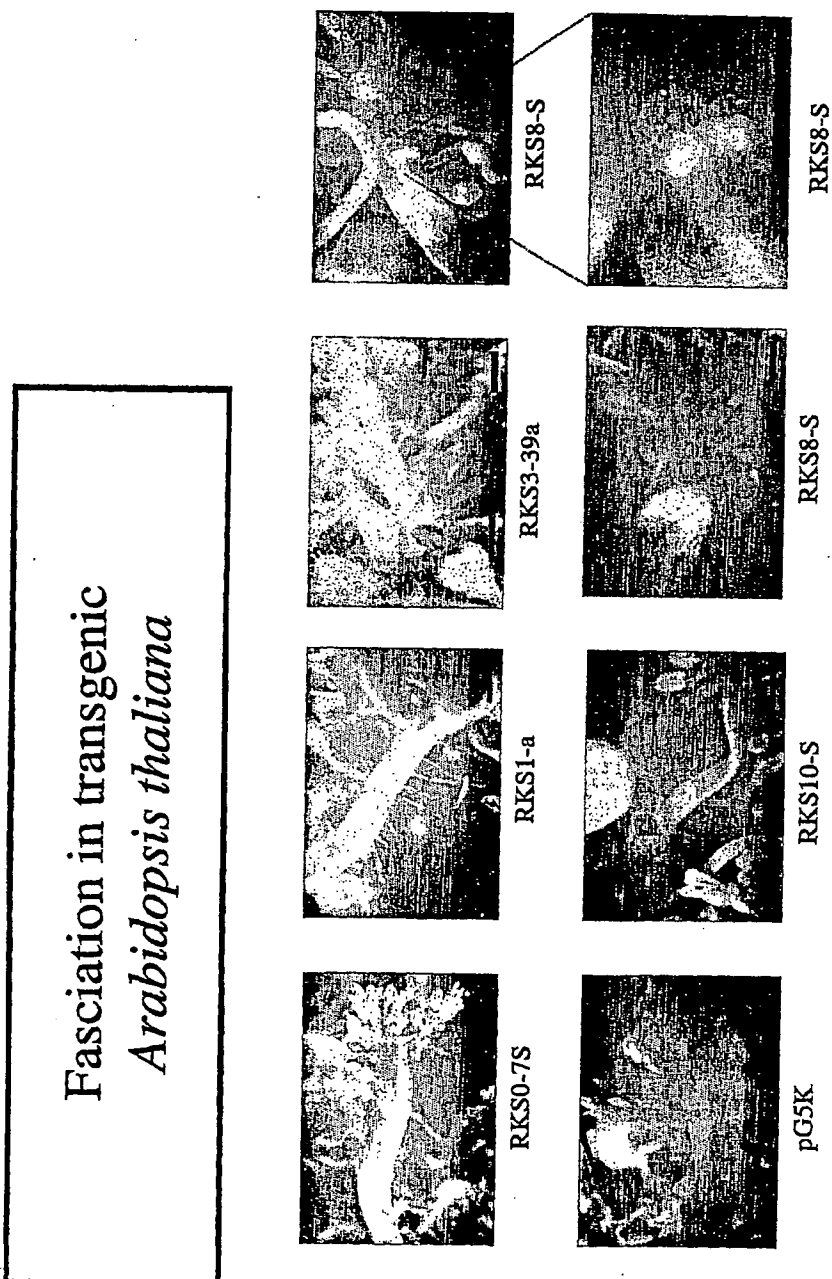


Fig. 20

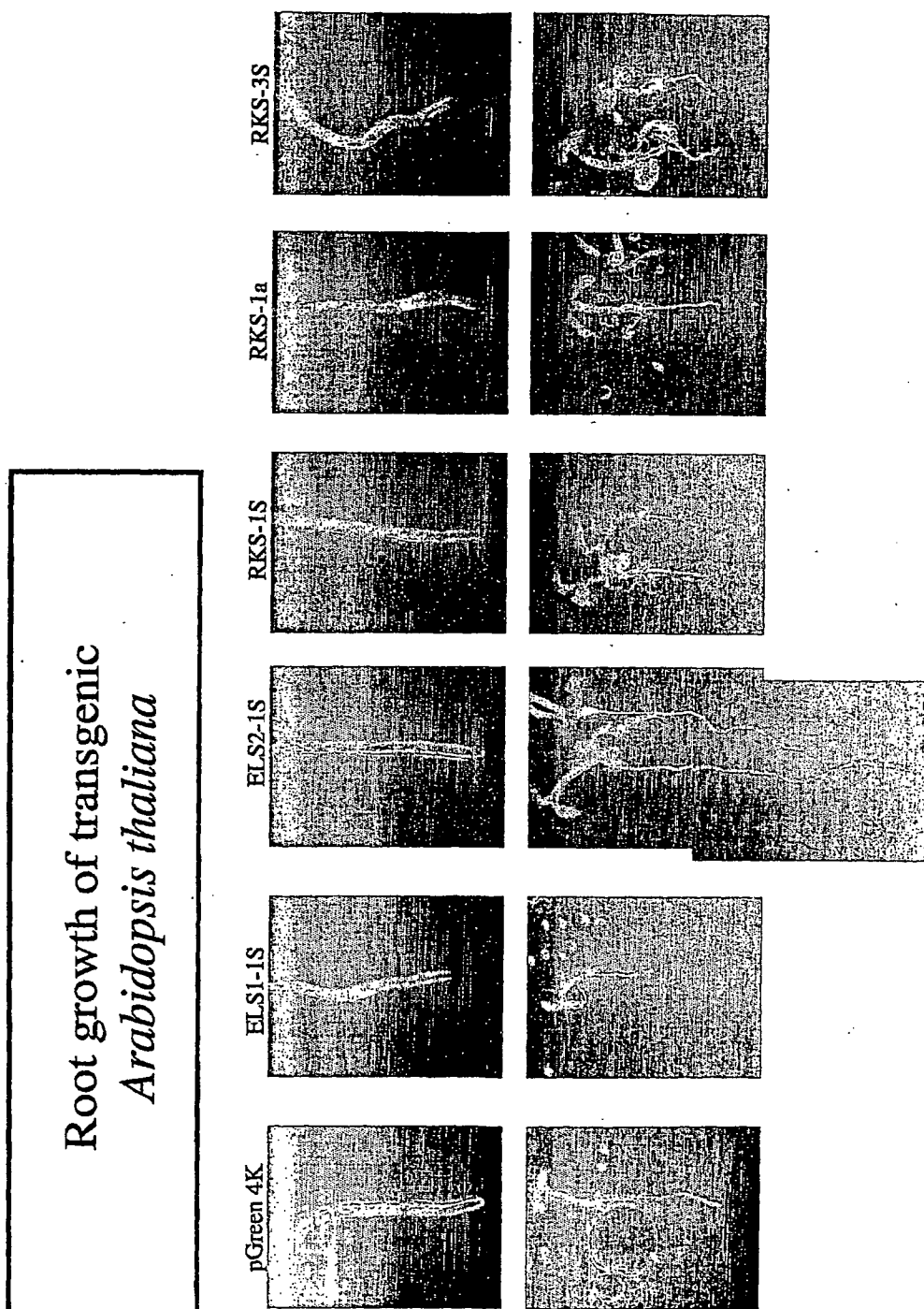


Fig. 21

Root growth of transgenic
Arabidopsis thaliana

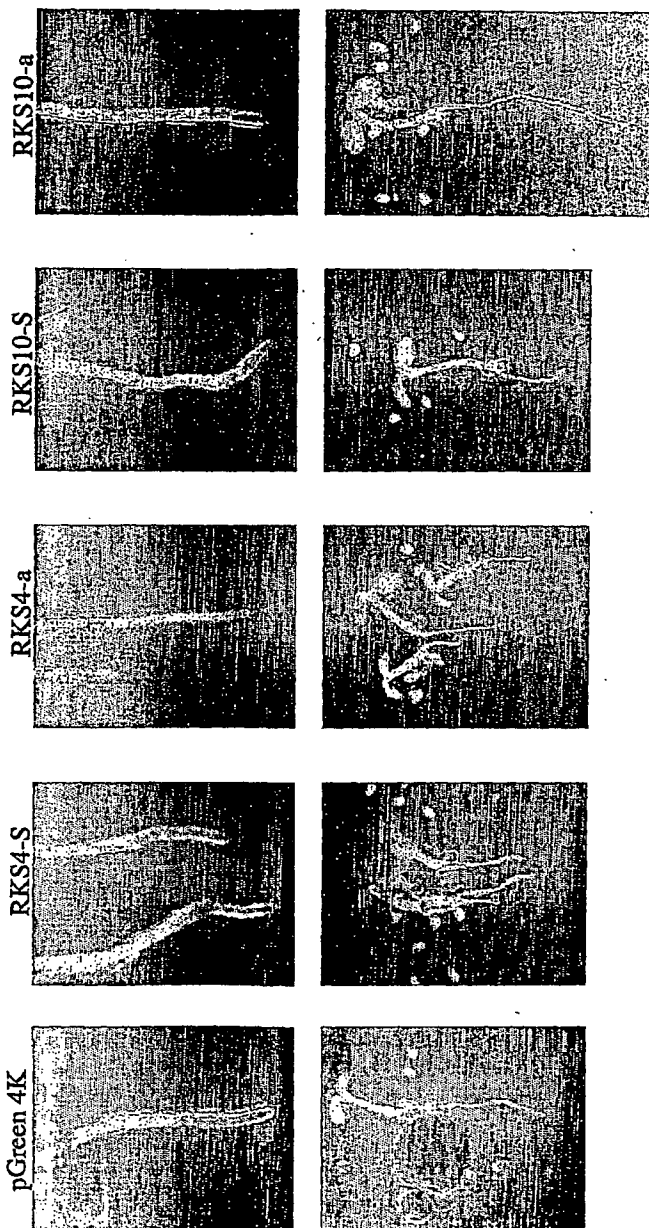
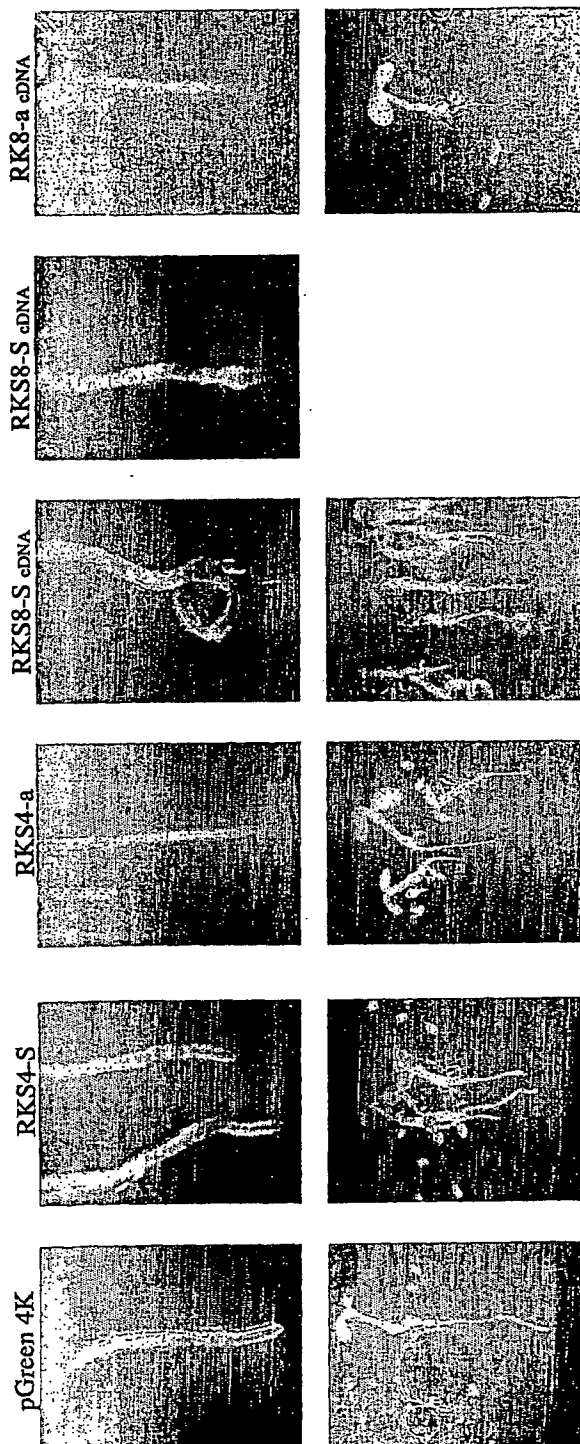


Fig. 22

Root growth of transgenic
Arabidopsis thaliana



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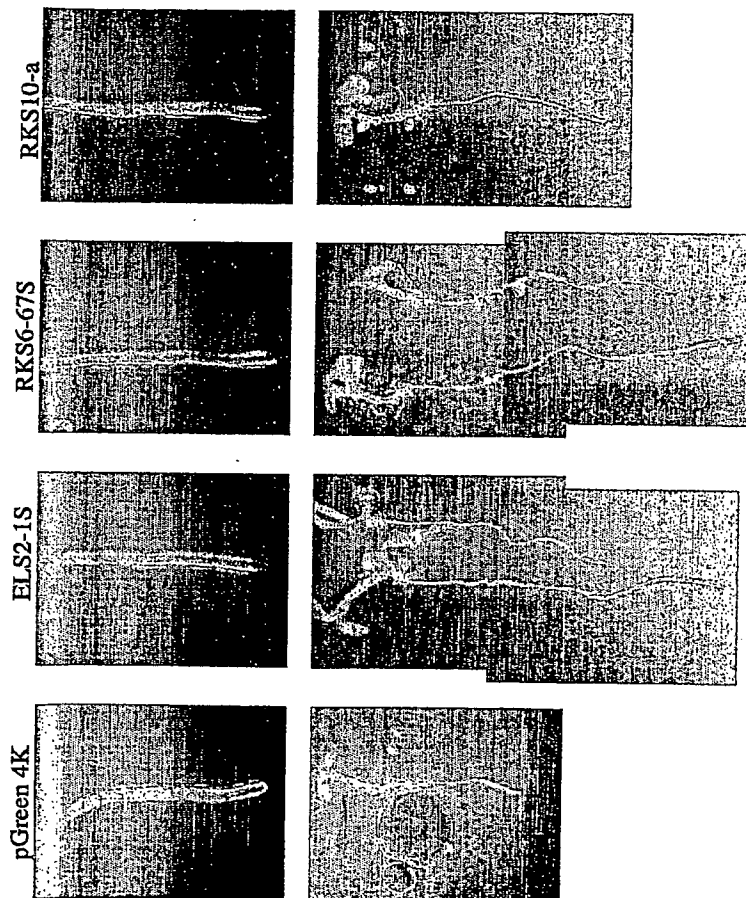
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Fig. 23

Root growth of transgenic
Arabidopsis thaliana



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Fig. 24

Transgenic *Arabidopsis thaliana*
 primary root length after 14 days
 of germination

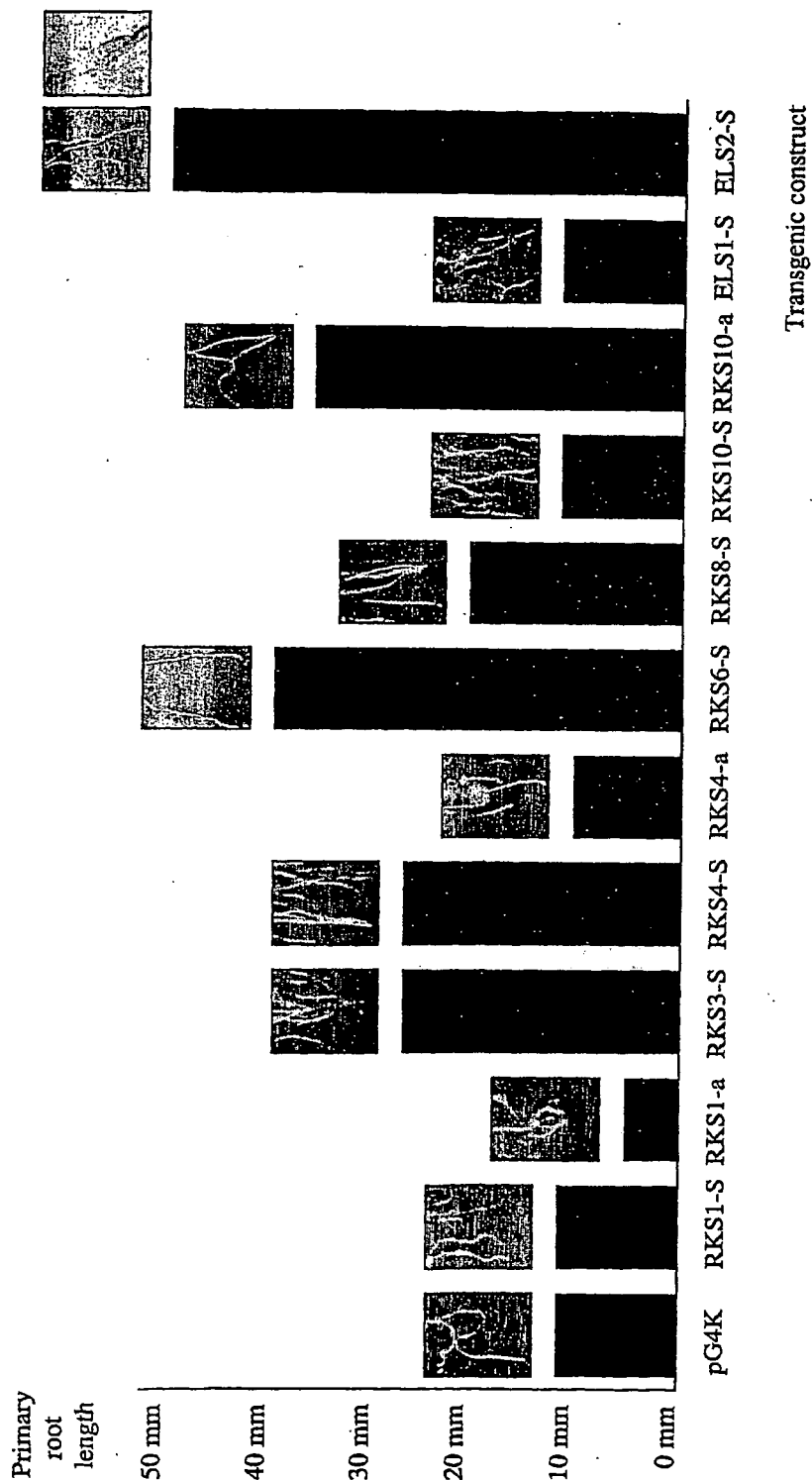


Fig. 25

Effects of RKS10 transgenic
constructs on plant development
of 45 days old *Arabidopsis* WS

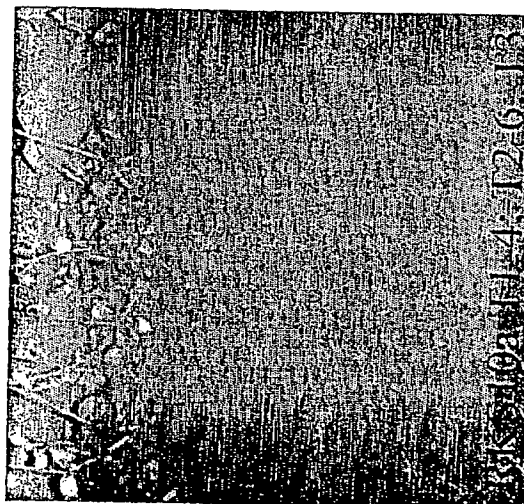
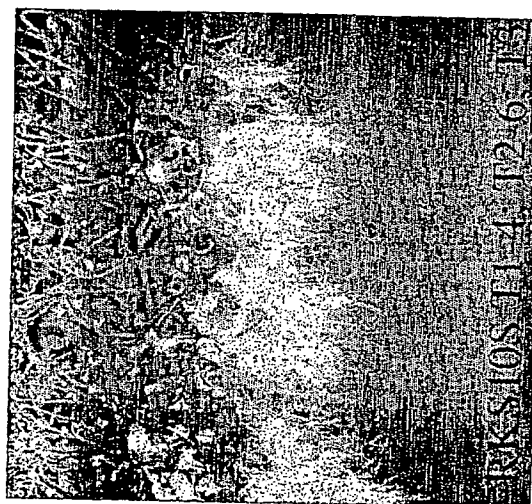
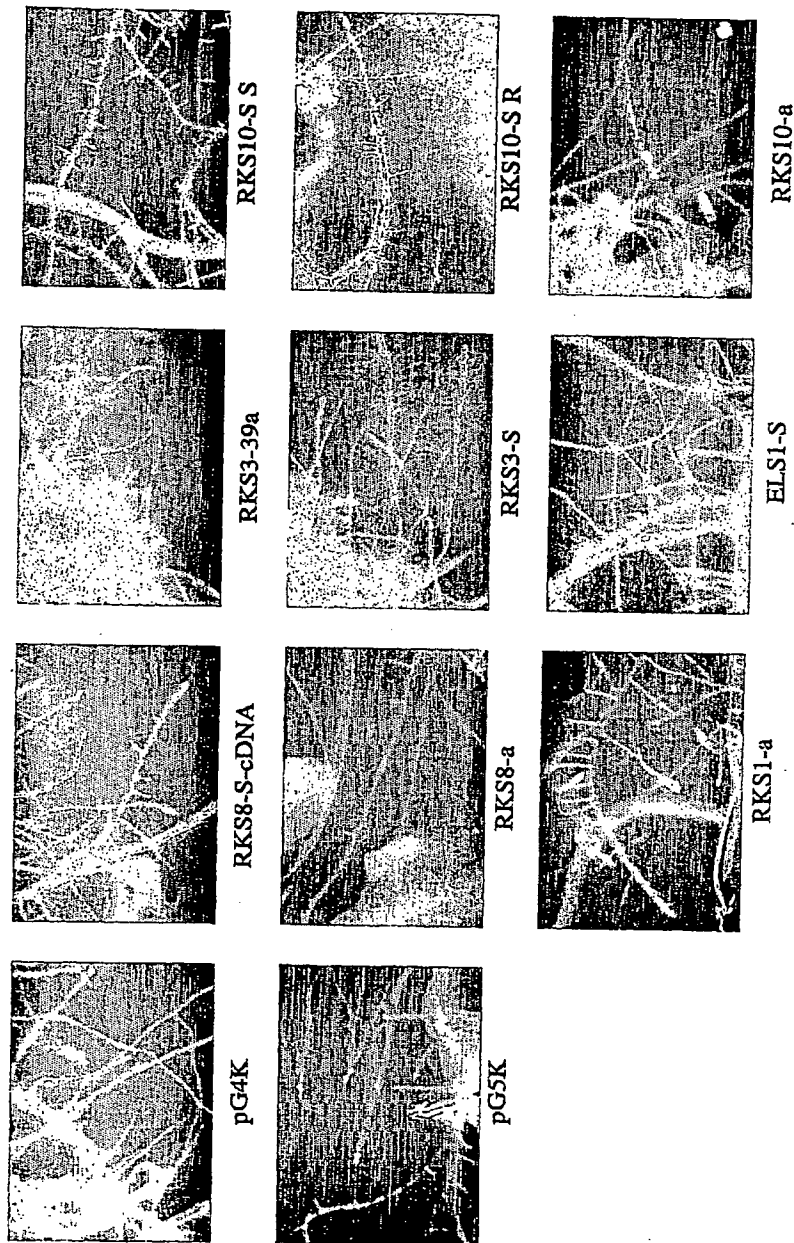


Fig. 26

Roots of Transgenic
Arabidopsis thaliana



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FIG

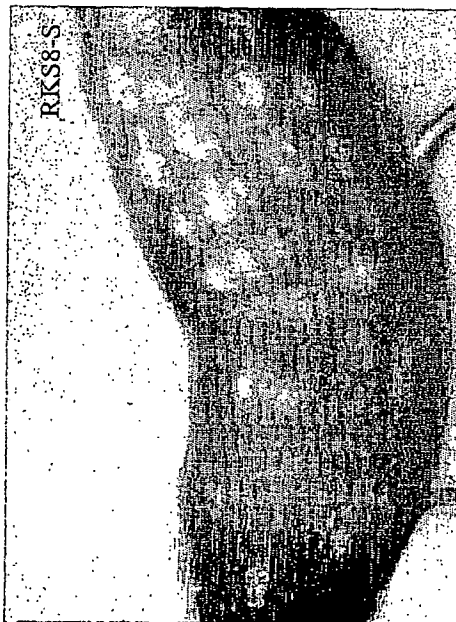
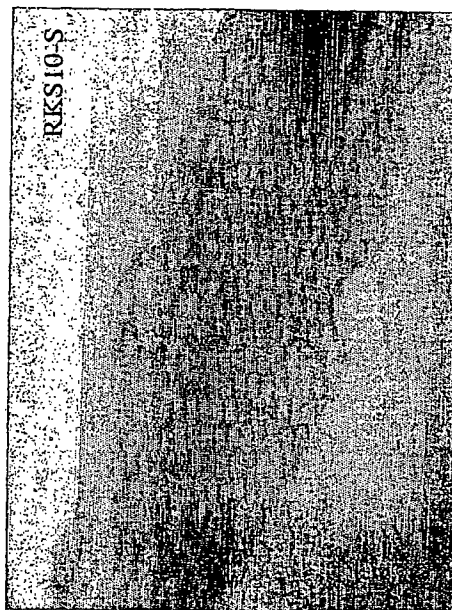
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Fig. 27

Root cells of transgenic
Arabidopsis thaliana



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Fig. 28

Influences of T1 transgenic
Arabidopsis WS plants

ELS-1-T1



RKS8-a-T1-10



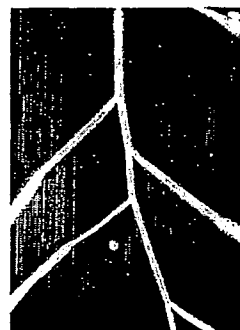
RKS10-a-T2



RKS10-S-T1-10



Control pGreen4K



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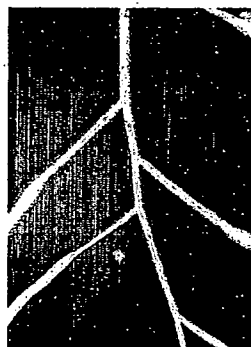
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Fig. 29

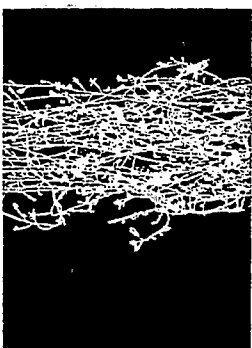
Influences of T1 transgenic
Arabidopsis WS plants



Control pG4K



RKS8-a-T1-10



RKS10-S-T1-10



Fig. 30

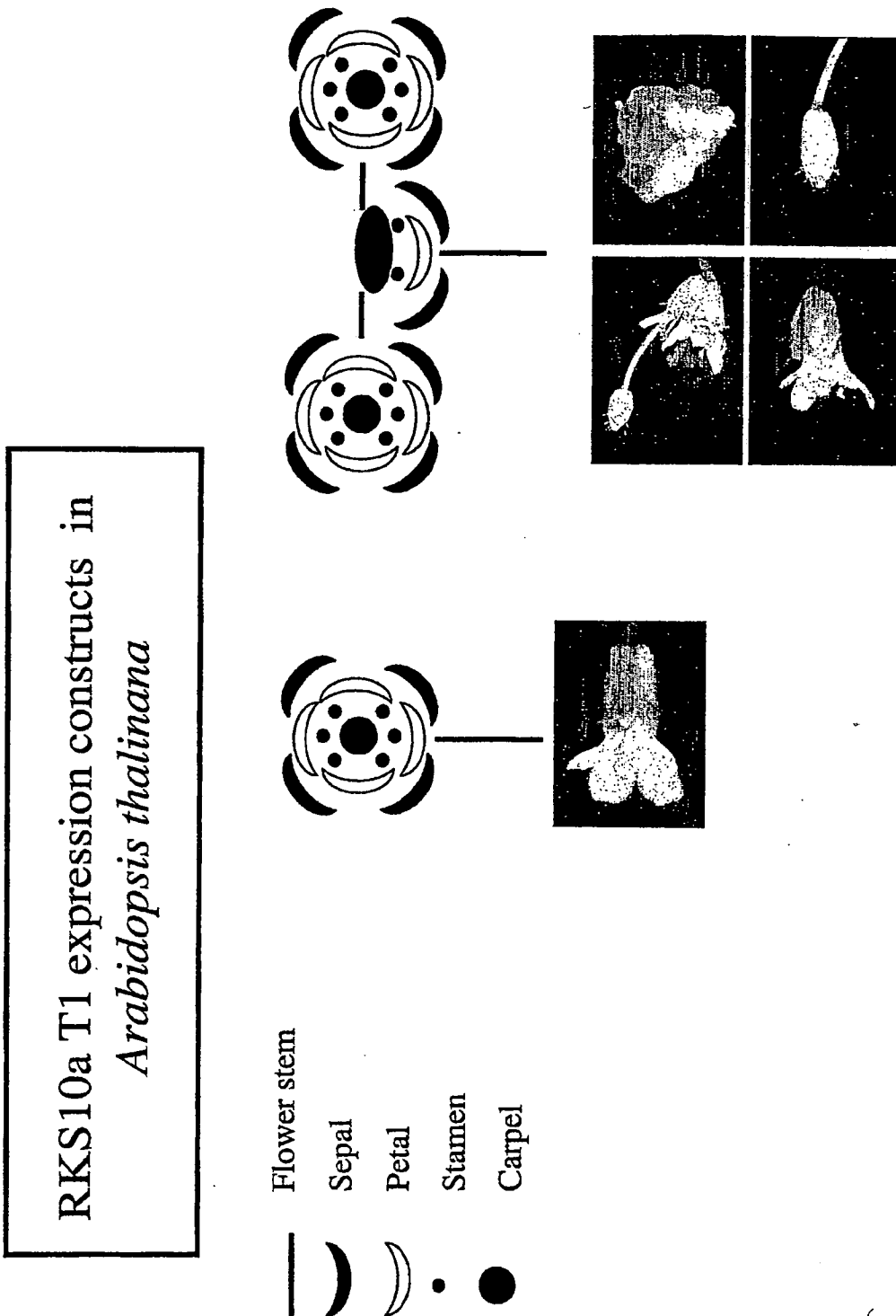
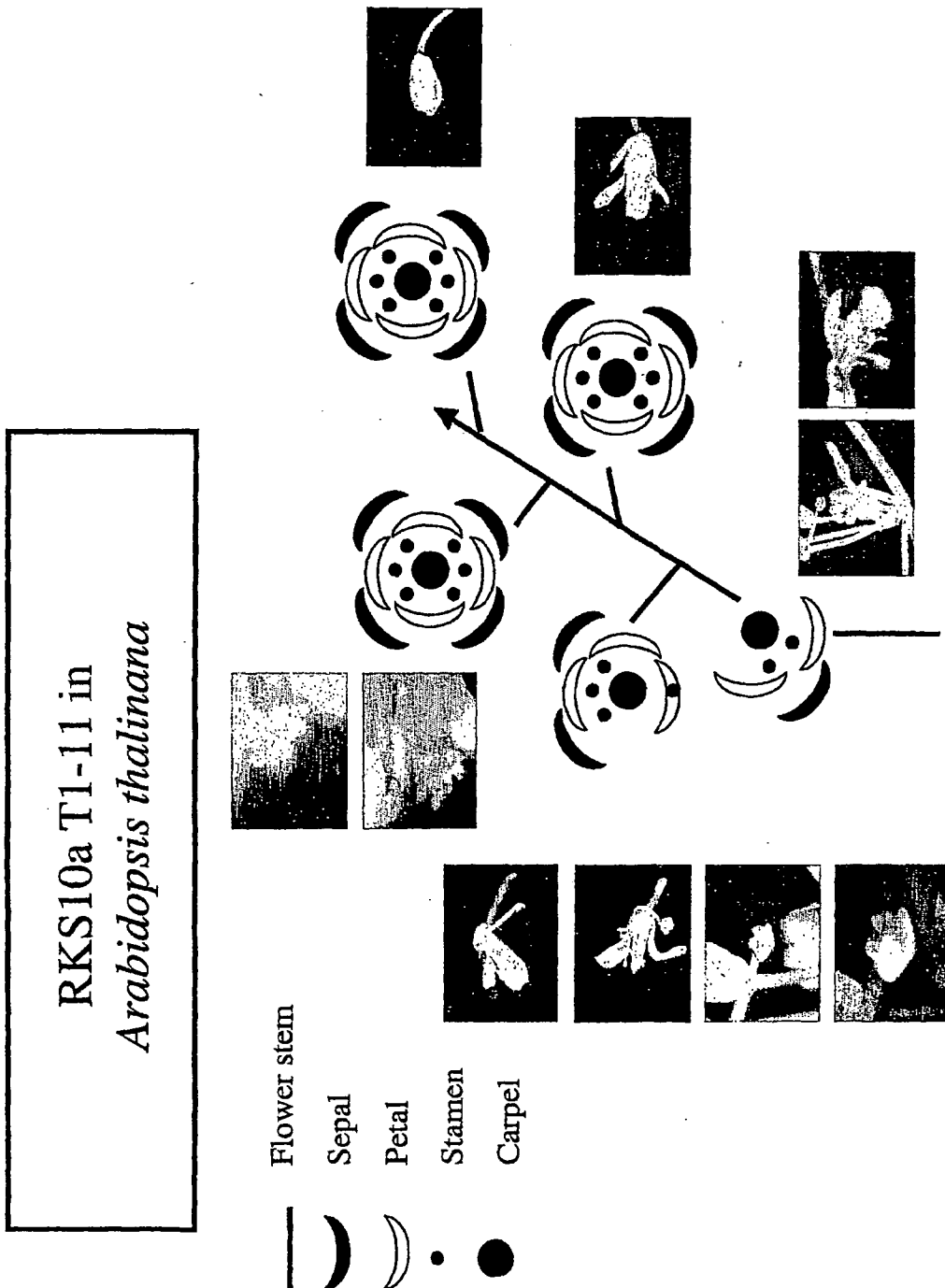


Fig. 31



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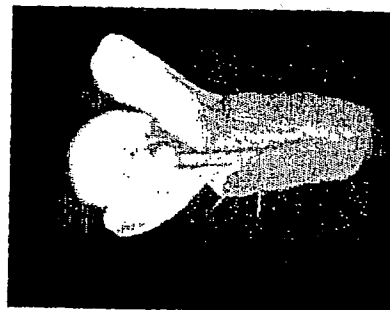
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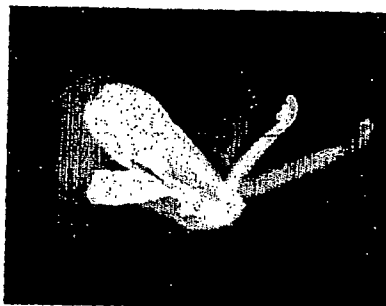
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Fig. 32

RKS10 antisense effects in
Arabidopsis thaliana



pGreen 4K



RKS10a T1-11



detail flower RKS10a T1-11



Fig. 33

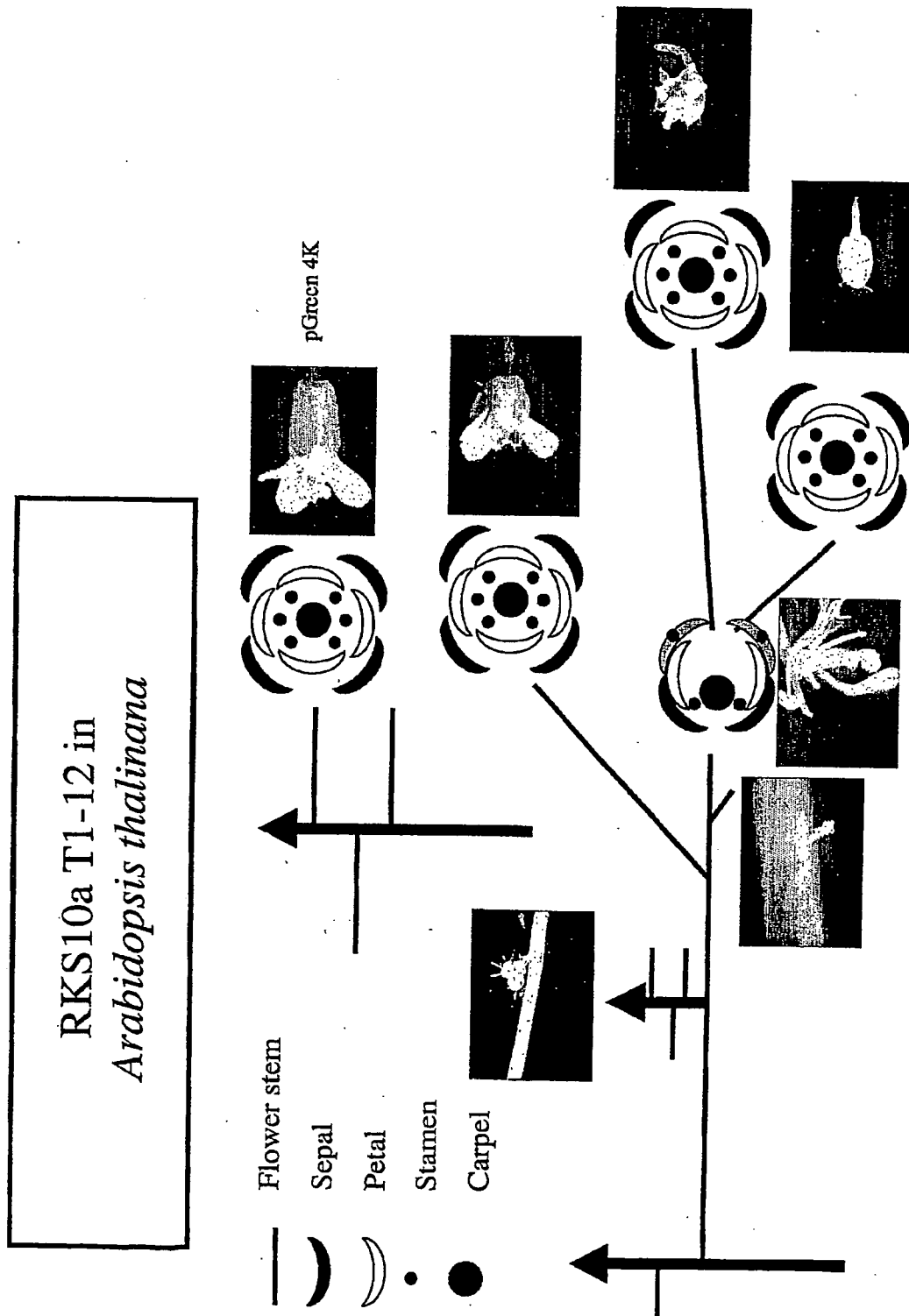
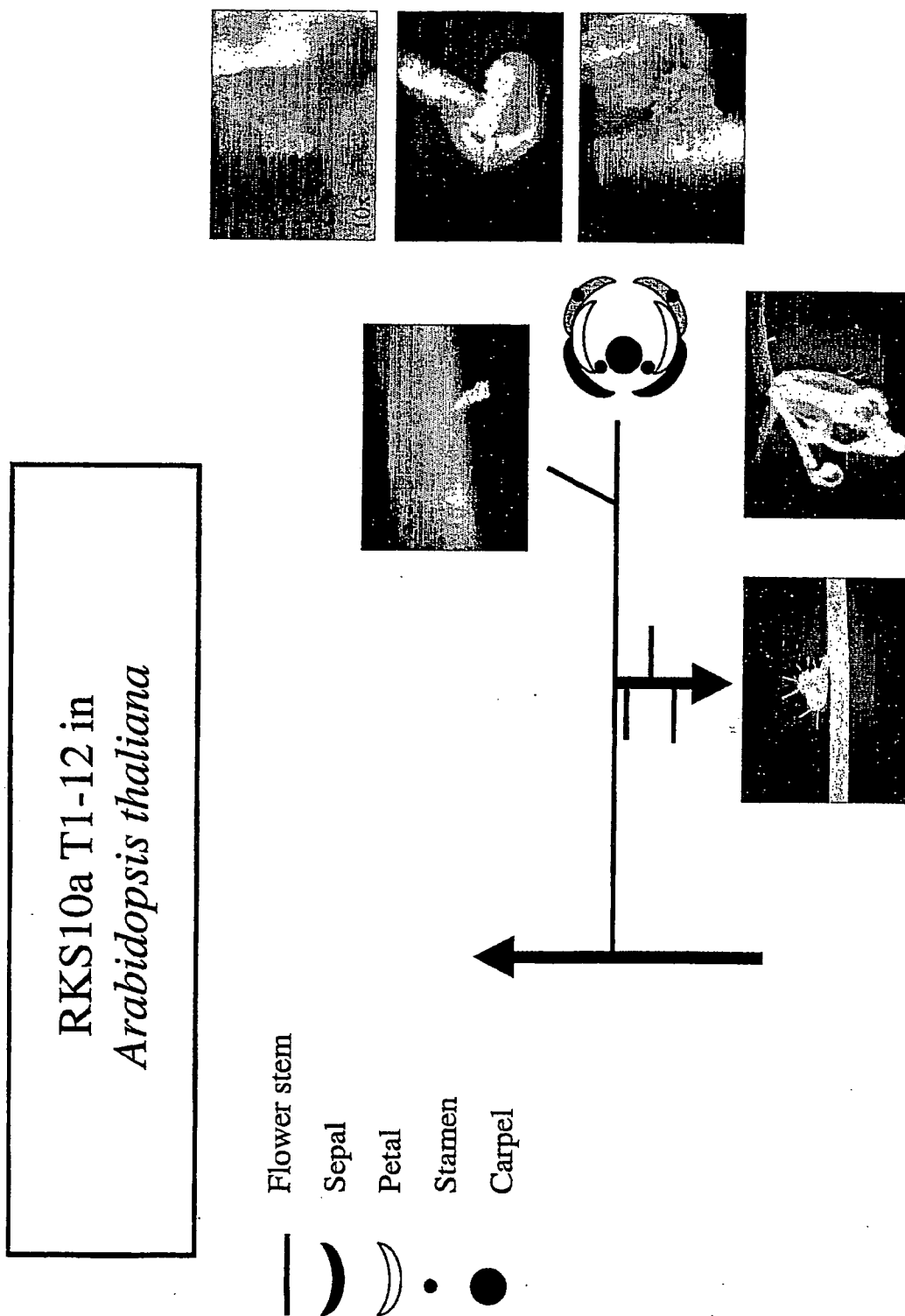


Fig. 34



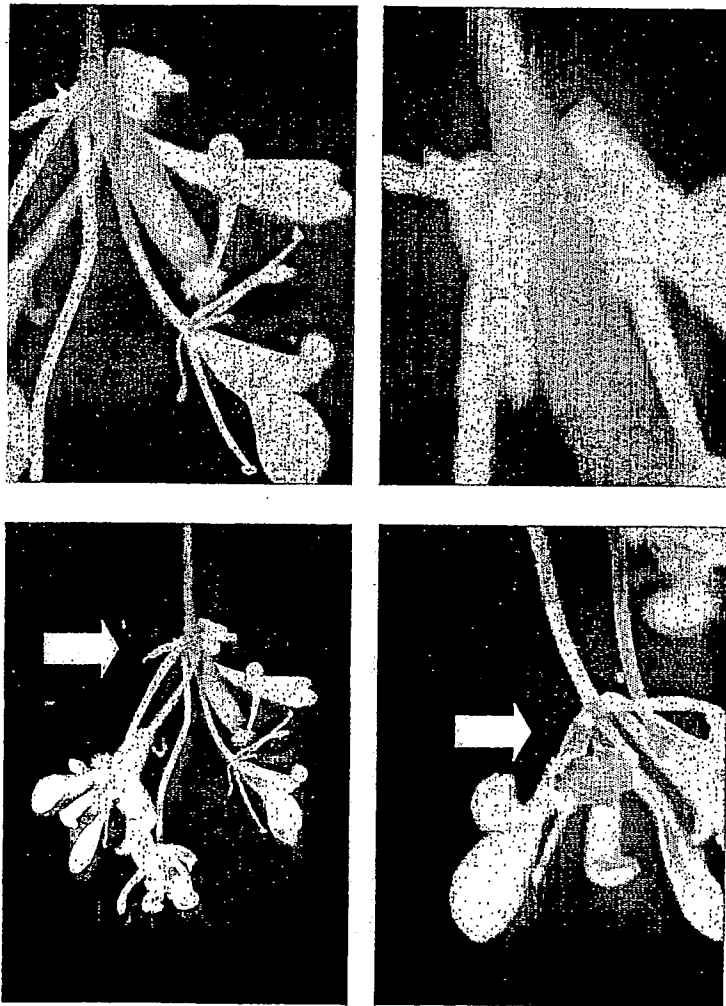
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Fig. 35

RKS13 regulates
flower meristem identity in
Arabidopsis thaliana



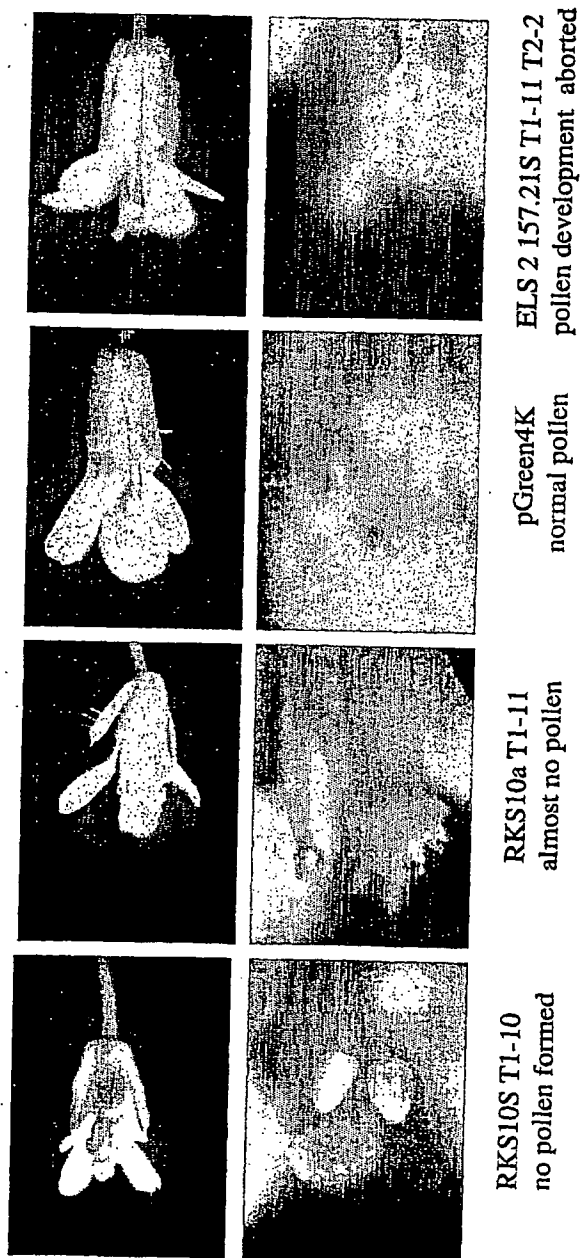
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Fig. 36

Male sterile transgenes in
Arabidopsis thaliana



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